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OM nucleic - nucleic search, using sw model

Run on: December 9, 2002, 09:18:16 ; Search time 1242.59 seconds
(without alignments)
13865.275 Million cell updates/sec

Title: US-09-905-114-1
Perfect score: 592
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_ov:*
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32: em_hcg_other:*
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35: em_hcg_rdd:*
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37: em_hcg_vrt:*
38: em_sy:*
39: em_hugo_hum:*
40: em_hugo_mus:*
41: em_hugo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	476.8	80.5	1023	AX329742	AX329742 Sequence
2	476.8	80.5	1023	AX332286	AX332286 Sequence
3	476.8	80.5	1023	AX332789	AX332789 Sequence
4	476.8	80.5	1023	AX410746	AX410746 Sequence
5	476.8	80.5	1023	HSUS6814	US6814 Human DNase
6	476.8	80.5	1067	BC015831	BC015831 Homo sapi
7	476.8	80.5	1079	AF047354	AF047354 Homo sapi
8	475.2	80.3	1108	HSU75744	U75744 Homo sapien
9	459.2	77.6	1131	AF039852	AF039852 Rattus no
10	459.2	77.6	1417	RNU75689	U75689 Rattus norv
11	452.8	76.5	1208	AR047845	AR047845 Sequence
12	452.8	76.5	1208	E11687	E11687 cDNA encodi
13	435.2	73.5	941	MMU76110	U76110 Mus musculu
14	435.2	73.5	1124	AF047355	AF047355 Mus muscu
15	433.6	73.2	2110	BC012671	BC012671 Mus muscu
16	387.2	65.4	1223	AX400016	AX400016 Sequence
17	280.8	47.4	1295	AF059612	AF059612 Xenopus 1
18	173.2	29.3	1295	BTNPANDNAI	AJ001538 Bos tauru
19	172.2	29.1	868	AF311922	AF311922 Bos tauru
20	171.4	29.0	392	AX330074	AX330074 Sequence
21	171.4	29.0	392	AX407983	AX407983 Sequence
22	163.2	27.6	1210	AB038776	AB038776 Rana cete
23	160.6	27.1	1283	AB041732	AB041732 Cynops py
24	154	26.0	1161	D82875	D82875 Oryctolagus
25	152.2	25.7	1312	BC014718	BC014718 Mus muscu
26	152.2	25.7	1337	BC030394	BC030394 Mus muscu
27	151	25.5	1297	AB048832	AB048832 Sus scrof
28	150.8	25.5	1156	RNDES0XI	X56060 Rat mRNA fo
29	150.8	25.5	1184	AF397151	AF397151 Rattus no
30	150.8	25.5	1313	AF397150	AF397150 Rattus no
31	150.6	25.4	1180	D83038	D83038 Mus musculu
32	149.4	25.2	1039	AX030575	AX030575 Sequence
33	149.4	25.2	1039	AX030591	AX030591 Sequence
34	149.4	25.2	1039	AX268671	AX268671 Sequence
35	149.4	25.2	1039	HMUNDAISEI	M55983 Human DNase
36	149.4	25.2	1149	BC029437	BC029437 Homo sapi
37	149.4	25.2	2054	HSR298844	AJ298844 Homo sapi
38	148.4	25.1	1066	AB013751	AB013751 Gallus ga
39	147.8	25.0	783	AX268673	AX268673 Sequence
40	147.8	25.0	858	AX268675	AX268675 Sequence
41	147.8	25.0	1039	AR019468	AR019468 Sequence
42	147.8	25.0	1548	AX268721	AX268721 Sequence
43	147.8	25.0	1548	AX268722	AX268722 Sequence
44	147.8	25.0	1554	AX268701	AX268701 Sequence
45	147.8	25.0	1554	AX268702	AX268702 Sequence

ALIGNMENTS

RESULT 1
AX329742 LOCUS AX329742 1023 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 251 from Patent WO0194629.
ACCESSION AX329742
VERSION AX329742.1 GI:18102720
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Young, P.E., Augustus, M., Carter, K.C., Edner, R., Endreess, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
TITLE

Pred. No. is the number of results predicted by chance to have a

JOURNAL	gene sets	BASE COUNT	312 a	244 c	240 g	227 t
FEATURES	Patent: WO 0194629-A 251 13-DEC-2001; Avalon Pharmaceuticals (US) Location/Qualifiers 1..1023 /organism="Homo sapiens" /db_xref="taxon:9606"	312 a	244 c	240 g	227 t	
ORIGIN						
Query Match	80.5%; Score 476.8; DB 6; Length 1023;					
Best Local Similarity	87.8%; Pred. No. 1.7e-119;					
Matches	520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;					
Qy	1 GAGAGCTAAACCGAAATTCAAGAAAGGCATAAATCAATCAATGATGATTAGCTCTCGC 60					
Db	241 GAGAAGCTGAACAGAAATTCAGAGGAGGCATTAACGTCACAACTATGTGATTAGCTCTCGG 300					
Qy	61 CTTGGAAGAAACACATATATAAGAAACAGTATGCTTTCTCTATAAGAAAGAGCTAGTGCT 120					
Db	301 CTTGGAAGAAACACATATATAAGAAACATATGCTTTCTCTACAGGAAAGCTGGTGCT 360					
Qy	121 GTAAAAACAAGCTACCTCTACCAAGCACTATCAGGCTGGAGACGAGAGATGTTTCCAGG 180					
Db	361 GTGAAGAGGAGTTATCACTACCTACCTACAGTATCAGGATGAGACGAGATGTTTCCAGG 420					
Qy	181 GAACCCCTTTGCTGCTGGTTCCAGTCACCTACACCGCTGTCAAGGACTTCGTGATTGTC 240					
Db	421 GAGCCCTTTGCTGCTGGTTCCAACTCTCCCACTGCTGTCAAGAGACTTCGTGATTATC 480					
Qy	241 CCCCTGCACACACCCCTGAGACATCCGTTAGAGAGATTGATAGCTGGCTGATGCTAC 300					
Db	481 CCCCTGCACACACCCACAGACATCCGTTAAGGAGATCGATGATGTTGGTTGAGTCTAC 540					
Qy	301 ACAGATGTGAAGCTCGCTGGAATCGACAGAAATTTCAATTTTCATGGTGATCTCAATGCT 360					
Db	541 ACGGACGTGAACACACCGCTGGAAGCGGAGAAATTTCAATTTTCATGGTGATCTCAATGCT 600					
Qy	361 GGCTGCAGCTAGCTTCCCAAGAAGCCCTGGAAGGACATCCGCTTGAGGACGAGACCCCAAG 420					
Db	601 GGCTGCAGCTAGCTTCCCAAGAAGCCCTGGAAGGACATCCGCTTGAGGACGAGACCCCAAG 660					
Qy	421 TTGCTTTGCTGATCGGGGACCAAGAGGACACACCGTCAAGAGAGACCAAACTCGCC 480					
Db	661 TTGTTTGGCTGATCGGGGACCAAGAGGACACACCGTCAAGAGAGACCAAACTCGCA 720					
Qy	481 TATGACAGATCGTCTTAGAGGACAAATATGTCAACTCTGGTGGTCTCAATCAAAAC 540					
Db	721 TATGACAGATGCTCTTAGAGGACAAATATGTCAGTTCTGTGTTTCCAAAGTCAAAAC 780					
Qy	541 CTCGCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 592					
Db	781 AGTGTTTTTGACTTCCAGAAAGCTTACAAGCTGACTGAAGAGGAGGCCCTGG 832					
RESULT 2						
AX332286						
LOCUS	AX332286	1023 bp	DNA	linear	PAT 09-JAN-2002	
DEFINITION	Sequence 2795 from Patent WO0194629.					
ACCESSION	AX332286					
VERSION	AX332286.1	GI:18122920				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.					
AUTHORS	1 Young P E., Augustus M., Carter, K.C., Ebner, R., Endress, G., Horrihan, S., Soppet, D.R. and Weaver, Z.					
TITLE	Cancer gene determination and therapeutic screening using signature gene sets					
JOURNAL	Patent: WO 0194629-A 2795 13-DEC-2001; Avalon Pharmaceuticals (US)					

BASE COUNT 312 a 244 c 240 g 227 t
ORIGIN

Query Match 80.5%; Score 476.8; DB 6; Length 1023;
Best Local Similarity 87.8%; Pred. No. 1.7e-119;
Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

1 GAAAGCTAAACGGAATTCAGAAAGGCAATACATACATATGATGATAGCTCCG 60
241 GAGAGCTGAACGAAATTCAGAGAGAGGCAATACATACATATGATGATAGCTCCG 300
61 CTGGAAGAAACATATATAAGAAACATATGCTTTCTCTATAAGAAAGTAGTGCT 120
301 CTGGAAGAAACATATATAAGAAACATATGCTTTCTCTATAAGAAAGTAGTGCT 360
121 GTAAACAAAGCTACCTCTACAGACTATCAGGCTGAGAGAGGAGATGTTTTCCAG 180
361 GTGAAGAGAGTATACATACATGACTATCAGAGATGAGAGAGGAGATGTTTTCCAG 420
181 GAACCTTTGTGTGTTGTTCCAGTACACCTACACCGCTGCAAGAGCTCGTATGTC 240
421 GAGCCCTTTGTGTGTTGTTCCAGTACACCTACACCTGCTCTCAAGAGCTTGATATC 480
241 CCCCTGACACACACCCCTGAGACATCCGTTAGAGATGATGAGTGTGATGCTAC 300
481 CCCCTGACACACACCCCTGAGACATCCGTTAGAGATGATGAGTGTGATGCTAC 540
301 ACAGATGTGAACAGTGTGCTGGAATGACAGAAATTTCAATTTGATGCTGATGCT 360
541 ACAGAGTGAACAGTGTGCTGGAATGACAGAAATTTCAATTTGATGCTGATGCT 600
361 GGTGAGAGTACCTCCCAAGAGGCTGGAAGAGATCCGCTGAGAGAGAGAGAGAG 420
601 GGTGAGAGTACCTCCCAAGAGGCTGGAAGAGATCCGCTGAGAGAGAGAGAGAG 660
421 TTGCTTTGGCTGATCGGGGACCAAGAGACACCGCTGAGAGAGAGAGAGAGAG 480
661 TTGCTTTGGCTGATCGGGGACCAAGAGACACCGCTGAGAGAGAGAGAGAGAG 720
481 TATGACAGGATGTGCTTGAAGAGCAAGAAATGCTGATGCTGCTCAATCAAC 540
721 TATGACAGGATGTGCTTGAAGAGCAAGAAATGCTGATGCTGCTCAATCAAC 780
541 CTGCTCTTTGATTTCCAGAAAGCTTACAGGTTGCTGAATCGAAGGCCCTGG 592
781 AGTGTTTTGAATTCAGAAAGCTTACAGGTTGCTGAATCGAAGGCCCTGG 832

RESULT 4
LOCUS AX410746 1023 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 3393 from Patent WO0229103.
ACCESSION AX410746
VERSION AX410746.1 GI:21443451
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3393 11-APR-2002;
GENE LOGIC INC (US)
FEATURES
source 1.1023
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. U56814"

BASE COUNT 312 a 244 c 240 g 227 t
ORIGIN

Query Match 80.5%; Score 476.8; DB 6; Length 1023;
Best Local Similarity 87.8%; Pred. No. 1.7e-119;
Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

1 GAAAGCTAAACGGAATTCAGAAAGGCAATACATACATATGATGATAGCTCCG 60
241 GAGAGCTGAACGAAATTCAGAGAGAGGCAATACATACATATGATGATAGCTCCG 300
61 CTGGAAGAAACATATATAAGAAACATATGCTTTCTCTATAAGAAAGTAGTGCT 120
301 CTGGAAGAAACATATATAAGAAACATATGCTTTCTCTATAAGAAAGTAGTGCT 360
121 GTAAACAAAGCTACCTCTACAGACTATCAGGCTGAGAGAGGAGATGTTTTCCAG 180
361 GTGAAGAGAGTATACATACATGACTATCAGAGATGAGAGAGGAGATGTTTTCCAG 420
181 GAACCTTTGTGTGTTGTTCCAGTACACCTACACCGCTGCAAGAGCTCGTATGTC 240
421 GAGCCCTTTGTGTGTTGTTCCAGTACACCTACACCTGCTCTCAAGAGCTTGATATC 480
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481 CCCCTGACACACACCCCTGAGACATCCGTTAGAGATGATGAGTGTGATGCTAC 540
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361 GGTGAGAGTACCTCCCAAGAGGCTGGAAGAGATCCGCTGAGAGAGAGAGAGAG 420
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721 TATGACAGGATGTGCTTGAAGAGCAAGAAATGCTGATGCTGCTCAATCAAC 780
541 CTGCTCTTTGATTTCCAGAAAGCTTACAGGTTGCTGAATCGAAGGCCCTGG 592
781 AGTGTTTTGAATTCAGAAAGCTTACAGGTTGCTGAATCGAAGGCCCTGG 832

RESULT 5
LOCUS HSU56814 1023 bp mRNA linear PRI 24-JUL-1997
DEFINITION Human DNase1-like III protein (DNAS1L3) mRNA, complete cds.
ACCESSION U56814
VERSION U56814.1 GI:1399718
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 1023)
TITLE Rodriguez, A.M., Rodin, D., Nomura, H., Morton, C.C., Weremowicz, S. and
Schneider, M.C.
JOURNAL Identification, localization, and expression of two novel human
genes similar to deoxyribonuclease I
MEDLINE Genomics 42 (3), 507-513 (1997)
PUBMED 97349121
9205125
2 (bases 1 to 1023)
REFERENCE
AUTHORS Schneider, M.C. and Rodriguez, A.
TITLE Direct Substitution
JOURNAL Submitted (25-APR-1996) M.C. Schneider, Renal Division, Brigham and
Women's Hospital, 75 Francis Street, Boston, MA 02115, USA
FEATURES
source 1.1023
/organism="Homo sapiens"
/db_xref="taxon:9606"

RESULT 6	BC015831	1067 bp	mRNA	linear	PRI 29-OCT-2001
LOCUS	BC015831				
DEFINITION	Homo sapiens, deoxyribonuclease I-like 3, clone MGC:27146				
	IMAGE:4723725, mRNA, complete cds.				
ACCESSION	BC015831				

QY	241	CCCCGACACACACCCCTAGACATCCGTTAGAGATGATGAGCGTCAATGCTAC	300
Db	524	CCCCGACACACACCCCGAGACATCCGTTAGAGATGATGAGCGTCAATGCTAC	583
QY	301	ACAGATGTGAAACGTGCTGATGATGCAGAAATTCATTTATGAGGTACTTCAATGCT	360
Db	584	ACGGAAGTGAACACCCGCTGGAAGCGGAGAAATTCATTTATGAGGTACTTCAATGCT	643
QY	361	GGCTGACGTCACGTCGCCCAAGAGCGTTGGAAGACATCCGCTGAGACGGAACCCCAAG	420
Db	644	GGCTGACGTCACGTCGCCCAAGAGCGCTGGAAGACATCCGCTGAGACGGAACCCCAAG	703
QY	421	TTTCGTTGGTGATGTGGGACCAAGAGACACCACGGTCAAGAGACACAACTGCGCC	480
Db	704	TTTGTGTTGGCTGATGGGGACCAAGAGACACCACGGTCAAGAGACACCAACTGTGCA	763
QY	481	TATGACAGGATGTGCTTAGAGACAAAATATGTCAATCTGTGCTGCTCAATCAAC	540
Db	764	TATGACAGGATGTGCTTAGAGACAAAATGTCAATCTGTGCTGCCAAGTCAAC	823
QY	541	CTCGCTTTGATTTTCAGAAAGCTTACAGAGTGTCTGAATTCAGAGCCCTGG	592
Db	824	AGCTGTTTTCATTCAGAAAGCTTACAGAGTGTCTGAATTCAGAGCCCTGG	875

LOCUS	AF047354	1079 bp	mRNA	linear	PRI 16-SEP-1996
DEFINITION	Homo sapiens liver and spleen DNaase precursor (LSD) mRNA, complete cds.				
ACCESSION	AF047354				
VERSION	AF047354.1	GI:2905785			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1079) Baron,W.F., Pan,C.Q., Spencer,S.A., Ryan,A.M., Lazarus,R.A. and Baker,K.P.				
TITLE	Cloning and characterization of an actin-resistant DNaase I-like endonuclease secreted by macrophages				
JOURNAL	Gene 215 (2), 291-301 (1998)				
MEDLINE	96382522				
PubMed	9714828				
REFERENCE	2 (bases 1 to 1079) Baron,W.F., Pan,C.Q., Spencer,S.A., Ryan,A.M., Lazarus,R.A. and Baker,K.P.				
AUTHORS	Direct Submission Submitted (09-FEB-1998) Molecular Biology, Genentech Inc., 1 DNA Way, South San Francisco, CA 94080, USA				
TITLE	Location/Qualifiers				
FEATURES	I..1079				
SOURCE					

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    SVKEIDELVEVYTDYKHWKMAENFIEMGDNPAGCSYYPKKAMKIKRLRTDPRFWMLG
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/ evidence=experimental
131. 985
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/ product="liver and spleen DNaase"
BASE COUNT      330 a      260 c      252 g      237 t
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Query Match	80.5%	Score 476.8;	DB 9;	Length 1079;
Best Local Similarity	87.8%;	Pred. No. 1.7e-119;		
Matches 520; Conservative	0;	Mismatches 72;	Indels 0;	Gaps 0

QY	1	GAGAAAGCTAAACGGAAATTC	2AAGAAAGGCAATTA	CACTCAACTATGATTTG	CTCGC	60
Db	287	GAGAAAGCTAAACGGAAATTC	2AAGAAAGGCAATTA	CACTCAACTATGATTTG	CTCGC	346
QY	61	CTTGGAAAGAAACATATATAA	AGAAACAGTATCGCTTCT	CTATTAAGAAAGCAAGCTAG	TGCT	120
Db	347	CTTGGAAAGAAACATATATAA	AGAAACATATATGCTTTCT	CTAACAAGAAAGCTGATG	TCT	406
QY	121	GTAAACAAACCTACCTTAC	CAAGCATATCAGGCTGGA	ACGACAGATGTGTTTTCC	AG	180
Db	407	GTGAAGAGAGATTATCACT	ATACCAATGACTATCAGAT	GTAGAGACGACAGATGTG	TTTCCAG	466
QY	181	GAAACCTTTGTGTGTGTTCC	AGTCAGTACCTTACACCG	GTGTCAAGACCTTGSTGAT	GTTC	240
Db	467	GAGCCCTTTGTGTGTGTTCC	AGTTCCTTCCACATGCTGT	GTCAAAAGACTTGTGTAT	TATTC	526
QY	241	CCCCGTGACACACACCCCT	GTAGACATCCGTTAGAG	AGATTTGATGAGCTGGCTAT	TTCTAC	300
Db	527	CCCCGTGACACACACCCCA	GTAGACATCCGTTAAGAG	ATGATGATGATGTGTTG	ATGAGGTCTAC	586
QY	301	ACAGATGTGAAACGTCCG	TTGGAATGCAAGAAATTT	CATTTTCATATGAGGTCA	TGCT	360
Db	587	ACGACGCGAAACACCGCT	GTGAAAGCGGAGAAATTT	CAATTTTCATATGAGGTCA	TGCT	646
QY	361	GGCTGCAGCTACGATCCCC	CAAGAAAGGCGCTGAA	AGGACATCCGCTGTAGGA	ACGACCCCAAG	420
Db	647	GCTGCAGCTACGATCCCC	CAAGAAAGGCGCTGTAG	GAAGAAACATCCGCTGTAG	GAACGACCCCAAG	706
QY	421	TTTCCTTTGGCTGATCGG	GGGAGCAAGAGGACACCA	ACGCTCAAGAAAGACACA	AACTGCGCC	480
Db	707	TTTCTTTTGGCTGATCGG	GGGAGCAAGAGGACACCA	ACGCTCAAGAAAGACACA	AACTGTGCA	766
QY	481	TATACACGATCGTGTCTTA	GAGACAAATATTTGTCAA	CTGTGCTGTCTCAATCA	AAAC	540
Db	767	TATACACGAGATTGCTT	AGAGACAAGAAATTCGT	CACTGTCTGTGTTCCCA	AGCTCAAC	826
QY	541	CTGCTCTTTGATTTCC	AGAAAGCTTACAGGTGT	CTGAATGGAAGCCCTCG	592	
Db	827	AGTGTCTTTTGTCTTCA	AGAAAGCTTACAGGTGT	CTGAATGGAAGCCCTCG	878	

RESULT	8
LOCUS	HSU75744
DEFINITION	Homo sapiens DNase gamma mRNA, complete cds.
ACCESSION	U75744
VERSION	U75744.1 GI:3236319
KEYWORDS	.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 1108)
TITLE	Shiockawa,D., Hirai,M. and Tanuma,S. cDNA cloning of human DNase gamma: chromosomal localization of its gene and enzymatic properties of recombinant protein
JOURNAL	Apoptosis 3 (2), 89-95 (1998)
REFERENCE	2 (bases 1 to 1108)
AUTHORS	Shiockawa,D. and Tanuma,S.
TITLE	Direct Submssion
JOURNAL	Submitted (23-OCT-1996) Biochemistry, Science Univ. of Tokyo,

Shinjuku-ku Ichigaya Funagawaracho, Tokyo 162, Japan

FEATURES
source
Location/Qualifiers
1. .1108
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VEPKLQSSRAFTNSKSVTLRKTKSKRS"
BASE COUNT 329 a 261 c 271 g 247 t
ORIGIN

Query Match 80.3%; Score 475.2; DB 9; Length 1108;
Best Local Similarity 87.7%; Pred. No. 4.7e-119;
Matches 519; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
Qy 1 GAGAGCTAAACGGAAATTCAGAAAGGCATACATCAACTATGTGATTAGCTCTCGC 60
Db 309 GAGAGCTGAACAGAAATTCAGGAGAGGCATACGTTCAACTATGTGATTAGCTCTCG 368
Qy 61 CTGGAAGAAACACATATAAGAACAGTATGCTTTCTCTATAAGAAAGACTAGTGCT 120
Db 369 CTGGAAGAAACACATATAAGAACATATGCTTTCTCTACAGGAAGAACTGCTGCT 428
Qy 121 GTAAACAAAGCTACCTTACCAGACTATCAGGCTGGAGACGAGATGTGTTTCCAGG 180
Db 429 GTGAAGAGGAGTTATCACTACCATGACTATCAGGATGAGAGCGAGATGTGTTTCCAGG 488
Qy 181 GAACCTTTGTGCTGCTTCCAGTCACTACCCGTACACCGCTGTCAAGGACTTCTGATGTGC 240
Db 489 GAGCCCTTTGTGCTGCTTCCAACTCTCCCACTGCTGTCAAGAGACTTCTGATTTATC 548
Qy 241 CCCCTGCACACCCCTGAGACATCCGTTAGAGAGATTGATGCTGGCTGATGCTCTAC 300
Db 549 CCCCTGCACACCCCTGAGACATCCGTTAAGAGATCGATGATGTTGGTTGAGTCTAC 608
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Db 609 ACGGACGTGAACACCGCTGGAAGCGGAGAAATTTCAATTTTCATGGTGAATCAATGCC 668
Qy 361 GGCTGCAGCTAGTCCCAAGAGCCCTGGAAGAGCATCCGCTGAGGACGGACCCCAAG 420
Db 669 GGCTGCAGCTAGTCCCAAGAGCCCTGGAAGAACATCCGCTTGAAGACTGACCCCAAG 728
Qy 421 TTGCTTTGCTGATCGGGGACCAAGAGACACCCGCTCAAGAGAGACACAACTGGGCC 480
Db 729 TTGCTTTGCTGATCGGGGACCAAGAGACACCCGCTGAAGAGAGACCACTGTGCA 788
Qy 481 TATGACAGGATCGTCTTAGAGGCAAAATATTTGCAACTCTGTTGGTCTTCAATCAAAAC 540
Db 789 TATGACAGGATGCTCTTAGAGGCAAGAAATCGTCACTTCTGTTGTTCCCAAGTCAAAAC 848
Qy 541 CTCGCTTTGATTTCCAGAAAGCTTACAGGTTGCTGTAATCGAAGGCCCTCG 592
Db 849 AGTGTGTTTGAATTTCCAGAAAGCTTACAGCTGACTGAAGAGGAGGCCCTCG 900
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AF039852 1331 bp mRNA linear ROD 07-AUG-1998
LOCUS Rattus norvegicus DNase gamma, complete cds.
DEFINITION AF039852
ACCESSION AF039852
VERSION AF039852.1 GI:3395771
KEYWORDS

SOURCE
ORGANISMRattus norvegicus.
Rattus norvegicusEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1331)

AUTHORS Liu, Q. Y., Pandey, S., Singh, R. K., Lin, W., Ribecco, M.,
Borowoy-Borowski, H., Smith, B., LeBlanc, J., Walker, P. R. and
Sikorska, M.TITLE DNasey: a rat DNaseI-like gene coding for a constitutively
expressed chromatin-bound endonuclease

JOURNAL Biochemistry 37 (28), 10134-10143 (1998)

MEDLINE 9832537

PUBMED 9665719

REFERENCE 2 (bases 1 to 1331)

AUTHORS Liu, Q. Y., Singh, R. K., Lin, W. and Sikorska, M.

TITLE Direct Submission

JOURNAL Submitted (24-DEC-1997) Institute for Biological Sciences, National
Research Council, 1200 Montreal Road, Bldg. M-54, Box 4, Ottawa, ON
K1A 0R6, CanadaFEATURES
Location/Qualifiers

source

1. .1331

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

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153. .1085

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BASE COUNT 351 a 333 c 320 g 327 t
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Best Local Similarity 86.0%; Pred. No. 1.1e-114;

Matches 509; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

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Db 384 GAGAGCTGAATGGAACCTCAGAGAGACGACATACACTACGTTAGCTCTCGG 443

Qy 61 CTGGAAGAAACACATATAAGAACAGTATGCTTTCTTATAAGAAAAAGCTAGTGCT 120

Db 444 CTGGAAGAAACACATATAAGAACAGTATGCTTCTCTACAAGGAGAGCTGGTGCT 503

Qy 121 GTAAACAAAGCTACCTTACCAGCTATCAGCTGGAGACGACAGATGTGTTCCAGG 180

Db 504 GTGAAGGCAAAATACCTCTACCATGACTATCAGGATGGAGACACACGTTTTCAGG 563

Qy 181 GAACCCCTTTGCTGCTGTTTCCAGTCAACCTACACCGCTGTCAAGGACTTCGTTGATGTC 240

Db 564 GAGCCCTTTGCTGTTTGGTTCCAGGCCCTTCACTGCTGCCAAGNACTTCGTTGATGTC 623

Qy 241 CCCCTGCACACCCCTGAGACATCGTTTAGAGAGATTGATGAGCTGGCTGATGCTAC 300

Db 624 CCCCTGCACAACTCCTGAAACCTCCGTTTAAAGAGATAGATGAGCTGGCTGCTAC 683

Qy 301 ACAGATGTGAACGCTCGCTGGAATGCAGAGAAATTCATTTTCATGGTGACTTCAATGCT 360

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DB	864	TATGACAGGATGTGCTTGGCGACAAAGATATGATCACTGTGGTTCGCCGCTCAGT	923
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DB	924	GGCGCTTGTGACTTCAGAAACCTTATGAGTGTGTGGAAGAGAGCGCTCG	975
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DEFINITION	Rattus norvegicus DNaase gamma mRNA, complete cds.		
ACCESSION	U75689		
VERSION	U75689.1	GI:3220024	
KEYWORDS			
SOURCE			
ORGANISM	Rattus norvegicus.		
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	Euxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
	Rattus.		
REFERENCE	1 (bases 1 to 1417)		
AUTHORS	Shioikawa,D., Ohyama,H., Yamada,T., Takahashi,K. and Tanuma,S.		
TITLE	Identification of an endonuclease responsible for apoptosis in rat thymocytes		
JOURNAL	Eur. J. Biochem. 226 (1), 23-30 (1994)		
MEDLINE	95045594		
PUBMED	7957253		
REFERENCE	2 (bases 1 to 1417)		
AUTHORS	Shioikawa,D. and Tanuma,S.		
TITLE	Molecular cloning and expression of a cDNA encoding an apoptotic endonuclease DNaase gamma		
JOURNAL	Biochem. J. 332 (Pt 3), 713-720 (1998)		
MEDLINE	98285539		
PUBMED	9620874		
REFERENCE	3 (bases 1 to 1417)		
AUTHORS	Shioikawa,D. and Tanuma,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-OCT-1996) Biochemistry, Science Univ. of Tokyo, Shinjuku-ku Ichigaya funagawaracho, Tokyo 162, Japan		
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D	b	434	GAGAA	GCTGAATG	AAAATC	AACGAA	AGAACG	ACGATCA	ACTA	CGATTG	AGCTTC	GG	493				
O	y	61	CTTGA	AAAAACA	CATATA	TAAAGA	ACAGTA	TGCCTTTCT	ATAA	AAAAAA	AGCTAG	GTCT	120				
D	b	494	CTTG	AAGAAA	CAACA	TATATA	AGAA	AGTAGT	CCCTCT	CAAGAG	AAAGCT	GTGTCT	553				
O	y	121	GTAAA	CAAAAG	TACCTT	CAAC	CACTAT	CAGCTG	GGAG	AGCATGT	TTTTCC	AG	180				
D	b	554	GTGA	AGCAA	AAATAC	CTTACC	TACAT	CTATAC	AGATG	GAAC	ACAG	CGTGT	TTCCAG	613			
O	y	181	GAAC	CTTTGT	GTGTC	GTTC	GTCC	AGTCA	CCCTCA	CCGCTG	TCMA	GACTCT	GTGAT	TTGTC	240		
D	b	614	GAGC	CTTTGT	GTGTG	TTGTG	TTGCC	AGCG	CCCTTCA	CTGTG	CCAG	ACGAT	CTTG	CTGAT	TTGTC	673	
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D	b	794	GGCT	CAC	ACTAC	TGTC	CCCC	CAAG	AGGCTG	GAAG	AGCAT	CCGCTG	SAGAG	CGGAC	CCCC	CAAG	853
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D	b	854	TTTG	TTTG	CTGAT	TTGG	GGGA	CAAG	AGGAC	CA	CGTCA	AGAA	AGGAC	CAAA	CTG	CGCC	913
O	y	481	TATG	ACAG	ATCG	TGCTT	AGAG	AGAC	AAATAT	TTGT	CAACT	CTGTG	TGCTT	CAAT	CAAA	C	540
D	b	914	TATG	ACAG	ATCG	TGCTT	AGAG	AGAC	AAATAT	TTGT	CAACT	CTGTG	TGCTT	CAAT	CAAA	C	973
O	y	541	CTCG	CTTGT	GAATTT	CCA	AAAGCTT	ACAG	TGTTG	TCTGA	TGGA	AGG	CGCC	CTG	S	92	
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ACCESSION AR047845																	
VERSION AR047845.1 GI:5970188																	
KEYWORDS .																	
SOURCE Unknown.																	
ORGANISM Unclassified.																	
REFERENCE 1 (bases 1 to 1208)																	
AUTHORS Tanuma,S.-I.																	
TITLE Deoxyribonuclease																	
JOURNAL Patent: US 5821103-A 2 13-OCT-1998;																	
FEATURES Location/Qualifiers																	
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Qy 241 CCCGTGCACACCCCTGAGACATCCGTTAGAGATTTGATGAGCTGGCTGATGTTCTAC 300
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Db 783 GCGCTTTGACTTTCAGAAAGCTTATGAGTTGCTGGAAGAGGAGGCCCTGG 834

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DEFINITION specifically linker site of chromatin DNA.
E11687
ACCESSION E11687.1 GI:22025323
VERSION E11687.1
KEYWORDS JP 1996187079-A/1.
SOURCE Rattus rattus.
ORGANISM Rattus rattus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1208)
TANUMA YASUKAZU
NEW DEOXYRIBONUCLEASE
Patent: JP 1996187079-A 1 23-JUL-1996;
OS Rattus rattus (rat)
PN JP 1996187079-A/1
PD 23-JUL-1996
PF 06-SEP-1995 JP 1995255647
PR 06-SEP-1994 JP 94P 239518
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CC strandedness: Double;
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FT CDS 12. .944
FT /product='Novel deoxyribonuclease (DNase) gamma
FT which cut
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Best Local Similarity 85.3%; Pred. No. 6.4e-113;
Matches 505; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
Qy 1 GAGAGCTAAACCGAATTCAGAAAGGCATACATACAACTATGTGATTAGCTCTCGC 60
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Qy 61 CTTGGAAGAAACACATATAAAGAACAGTATGCCCTTCTTATAAAGAAAAGCTAGTGTCT 120
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Qy 541 CTCGCTTTGATTTCCAGAAAGCTTACAGGTTGCTGTAATCGAAGGCCCTGG 592
Db 783 GCGCTCTTGCATTTTCAGAAAGCTTATGAGTTGTTGGAAGAGGAGGCCCTGG 834

RESULT 13
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DEFINITION
ACCESSION U76110
VERSION U76110.1 GI:4098207
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 941)
Shiokawa, D., Hatanaka, T. and Tanuma, S.
Direct Submission
Submitted (24-OCT-1996) Biochemistry, Science Univ. of Tokyo,
Shinjuku-ku ichigaya funagawaracho, Tokyo 162, Japan
LOCATION/Qualifiers
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7. .939
CDS

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Dp	418	GAGCCCTTTGTGTGTGTTCCATTCCTCCCTTACTGTGTCAAGACCTTCGTATGTC	477
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ACCESSION	AF047355
VERSION	AF047355.1 GI:2905787
KEYWORDS	Mus musculus liver and spleen DNaase precursor (LSD)
SOURCE	cds.
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REFERENCE	Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS	1 (bases 1 to 1124) Baron, W.F., Pan, C.Q., Spencer, S.A., Ryan, A.M., Lazarus, R.A. and Baker, K.P.
TITLE	Cloning and characterization of an actin-resistant DNase I-like endonuclease secreted by macrophages
JOURNAL	Gene 215 (2), 291-301 (1998)
MEDLINE	98382522
PUBMED	9714828
REFERENCE	2 (bases 1 to 1124)
AUTHORS	Baron, W.F., Pan, C.Q., Spencer, S.A., Ryan, A.M., Lazarus, R.A. and Baker, K.P.
TITLE	Direct Submission
JOURNAL	Submitted (09-FEB-1998) Molecular Biology, Genentech Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES	Location/Qualifiers

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Best Local Similarity	83.4%; Pred. No. 4.1e-108;	
Matches 494; Conservative	0; Mismatches 98; Indels 0; Gaps 0	
QY	1 GAGAACTTAAAGGAATTCAGAAAAAGCGCTAAACATACATACATATGTGATTAGCTTCGC	60
DB	404 GAGAACTGTAAGGAATTCAGGAAGAGCAACAATACAACTATGTGATTAGCTTCGCA	463
QY	61 CTTGGAAGAAACACATATTAAGAACAGTATGCCCTTTCCTATTAAGAAAGACTAGTGTCT	120
DB	464 CTTGGAAGAAACACGTACAAAGAGCAGTATCCTTCCTGTACAAAGAGAGCTGCTGTCT	523
QY	121 GTTAAACAAAGCTACTCTTACACGACTATATAGCGCTGAGAGCAGCATGTGTTTCCAG	180
DB	524 GTGAAACAAAATATACACTACCATGACTCATATAGATGAGAGCAGACAGACGTGTTTCCAG	583
QY	181 GAACCTTTGTGGTCTGGTCCAGTCACTTACACCGGTGCAAGGACTCGTGAATGTC	240
DB	584 GAGCCCTTTGTGGTGTGTTCCATTCCTCCCTTATCTGCTGCAAGACTTCGTGATTGTC	643
QY	241 CCCCTGACACACACCCCTTGAGACATCCGTTAGAGAGATTATGAGCTGCTGATGCTTAC	300
DB	644 CCCCTGACACACAACCTCCGAGACCTCCGTTAAAGAGATAGATGAGCTGCTGATGCTTAC	703
QY	301 ACAGATGTCAAACTGCGCTGGAATGACAGAGATTCTATTTTCAATGGGTGACTCAATGCT	360
DB	704 ACGAGTGTGAGAAAGCAAGCAAGTGGAGACAGAAATTTCACTTTCATGGGTGATTTCAAGCC	763
QY	361 GGCTGACGCTACGTCCTCCAGAGAGCGCTGGAAGACATCCGCTGAGAGACGACCCCAAG	420

XX PI Zhang H, Ax RL, Bellin ME;
XX WPI; 2002-171803/22.
DR P-PSDB; AAE18281.
XX Novel amino acid and polynucleotide sequence for fertility associated
PT antigen useful for increasing stability of plasma membrane, acrosome
PT and other portions of sperm cell, and increasing fertility of mammals
PT
XX
XX Claim 1; Fig 6; 37pp; English.
XX The invention relates to bovine fertility associated antigen (FAA) and
CC its nucleic acid sequence. FAA is useful for increasing the stability of
CC the plasma membrane plus acrosome of a sperm cell and/or other portions
CC of a sperm cell, in particular mammalian sperm cell such as a sperm cell
CC from buffalo, cow, horse, mice, pig, sheep, human, avian sperm cell
CC including turkey or chicken sperm cell. FAA is also useful for increasing
CC the fertility of sperm from a mammal including buffalo, cow, horse, mice,
CC pig, sheep or human, or avian (chicken or turkey). FAA is added to the
CC suspension of sperm cells prior to preservation or prior to
CC administration of the sperm cells to a mammal in artificial insemination.
CC Alternatively, fertility of sperm from a mammal is increased by placing
CC FAA into a female's reproductive tract prior to deposition of the sperm
CC cells into the female's reproductive tract by copulation or artificial
CC insemination. The fertility of the male mammal is increased by injecting
CC FAA into the male mammal's reproductive tract. The present sequence is
CC bovine fertility associated antigen (FAA) partial cDNA.
XX
XX Sequence 592 BP; 170 A; 143 C; 142 G; 137 T; 0 other;
SQ

Query Match 100.0%; Score 592; DB 24; Length 592;
Best Local Similarity 100.0%; Pred. No. 6e-178;
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAAAGCTAAACGGAAATTCAGAAAGGCAATACATACAACTATGTGATTAGCTCTCGC 60
DB 1 GAGAAAGCTAAACGGAAATTCAGAAAGGCAATACATACAACTATGTGATTAGCTCTCGC 60

QY 61 CTTCGAGAAACACATATAAAGACAGTATGCCCTTTCTTATAAGAAAGCTAGTGCT 120
DB 61 CTTCGAGAAACACATATAAAGACAGTATGCCCTTTCTTATAAGAAAGCTAGTGCT 120

QY 121 GTAAACAAAGCTACCTCTACAGACTATCAGCTCGAGCGAGATGTGTTTCAGG 180
DB 121 GTAAACAAAGCTACCTCTACAGACTATCAGCTCGAGCGAGATGTGTTTCAGG 180

QY 181 GAACCCCTTTGTGGTCTGGTTCCAGTCAACCCCTACACCGCTGTCAAGGACTTCGTGATTGTC 240
DB 181 GAACCCCTTTGTGGTCTGGTTCCAGTCAACCCCTACACCGCTGTCAAGGACTTCGTGATTGTC 240

QY 241 CCCTGTGACACACCCCTGAGACATCCGTTAGAGAGATTGATGAGTGGCTGATGCTAC 300
DB 241 CCCTGTGACACACCCCTGAGACATCCGTTAGAGAGATTGATGAGTGGCTGATGCTAC 300

QY 301 ACAGATGGAACCTCGCTGGAATGCAGAGAAATTTTCATGCGGTGACTTCAATGCT 360
DB 301 ACAGATGGAACCTCGCTGGAATGCAGAGAAATTTTCATGCGGTGACTTCAATGCT 360

QY 361 GGCTGCAGTACGTCCCAAGAGCGCTGGAAGGACATCCGCTCGAGAGCGGACCCCAAG 420
DB 361 GGCTGCAGTACGTCCCAAGAGCGCTGGAAGGACATCCGCTCGAGAGCGGACCCCAAG 420

QY 421 TTGCTTTGGTGTATCGGGGACCAAGAGACACACCGTCAAGAGAGACAAACCTGGCC 480
DB 421 TTGCTTTGGTGTATCGGGGACCAAGAGAGACACACCGTCAAGAGAGACAAACCTGGCC 480

QY 481 TATGACAGGATCGTCTTAGAGGACAAATATTTGCTCACTCTGCTGCTCTCAATCAAC 540
DB 481 TATGACAGGATCGTCTTAGAGGACAAATATTTGCTCACTCTGCTGCTCTCAATCAAC 540

QY 541 CTCGCTTTGATTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 592

DB 541 CTCGCTTTGATTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 592
|||||

RESULT 2
AAD29089
ID AAD29089 standard; DNA; 671 BP.
XX
XX AAD29089;
AC
XX 16-MAY-2002 (first entry)
DT
XX
XX Bovine 22kDa recombinant FAA (rFAA) coding sequence.
DE
XX
XX Bovine; fertility associated antigen; FAA; sperm fertility; acrosome;
KW artificial insemination; plasma membrane; sperm cell; anti-infertility;
KW reproductive tract; ds.
XX
XX Bos sp.
OS
XX WO200206444-A2.
PN
XX
XX 24-JAN-2002.
PD
XX
XX 16-JUL-2001; 2001WO-US22097.
PF
XX
XX 14-JUL-2000; 2000US-218140P.
PR
XX
XX (ARIZ-) ARIZONA BOARD OF REGENTS.
PA
XX
XX Zhang H, Ax RL, Bellin ME;
PI
XX
XX WPI; 2002-171803/22.
DR
XX
XX Novel amino acid and polynucleotide sequence for fertility associated
PT antigen useful for increasing stability of plasma membrane, acrosome
PT and other portions of sperm cell, and increasing fertility of mammals
PT
XX
XX Claim 1; Fig 5; 37pp; English.
PS
XX
XX The invention relates to bovine fertility associated antigen (FAA) and
CC its nucleic acid sequence. FAA is useful for increasing the stability of
CC the plasma membrane plus acrosome of a sperm cell and/or other portions
CC of a sperm cell, in particular mammalian sperm cell such as a sperm cell
CC from buffalo, cow, horse, mice, pig, sheep, human, avian sperm cell
CC including turkey or chicken sperm cell. FAA is also useful for increasing
CC the fertility of sperm from a mammal including buffalo, cow, horse, mice,
CC pig, sheep or human, or avian (chicken or turkey). FAA is added to the
CC suspension of sperm cells prior to preservation or prior to
CC administration of the sperm cells to a mammal in artificial insemination.
CC Alternatively, fertility of sperm from a mammal is increased by placing
CC FAA into a female's reproductive tract prior to deposition of the sperm
CC cells into the female's reproductive tract by copulation or artificial
CC insemination. The fertility of the male mammal is increased by injecting
CC FAA into the male mammal's reproductive tract. The present sequence is
CC bovine 22kDa recombinant FAA (rFAA) coding sequence.
XX
XX Sequence 671 BP; 195 A; 166 C; 154 G; 156 T; 0 other;
SQ

Query Match 100.0%; Score 592; DB 24; Length 671;
Best Local Similarity 100.0%; Pred. No. 6.5e-178;
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAAAGCTAAACGGAAATTCAGAAAGGCAATACATACAACTATGTGATTAGCTCTCGC 60
DB 27 GAGAAAGCTAAACGGAAATTCAGAAAGGCAATACATACAACTATGTGATTAGCTCTCGC 86

QY 61 CTTCGAGAAACACATATAAAGACAGTATGCCCTTTCTTATAAGAAAGCTAGTGCT 120
DB 87 CTTCGAGAAACACATATAAAGACAGTATGCCCTTTCTTATAAGAAAGCTAGTGCT 146

QY 121 GTAAACAAAGCTACCTCTACAGGTTGTCTGAATCGAAGGCCCTGG 180

Db 480 AACTGGCGCTATGACAGGATCGTCTAGAGGACAAATATTTGTCAACTCTGGTGGTCT 539

QY 532 CAATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGG 570

Db 540 CAATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGG 578

RESULT 4

AAS17901

ID AAS17901 standard; cDNA; 556 BP.

AC AAS17901;

XX

XX

DT 26-MAR-2002 (first entry)

XX

DE Partial cDNA encoding human fertility-associated antigen (FAA), HCl.

XX

KW Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome;

KW reproductive fitness; single nucleotide polymorphism; SNP; human;

KW HCl; SS.

XX

OS Homo sapiens.

XX

XX

FH Key Location/Qualifiers

FT CDS 1..555

FT /*tag= a

FT /product= "Human FAA"

FT /note= "Human fertility-associated antigen, HCl"

FT /partial

FT /note= "No start or stop codon given"

FT /transl_except= (pos:1..3, aa:KVIKRCDIILLWEIKDS)

FT /transl_except= (pos: 253..255, aa:S)

XX

XX

PN WO200176529-A2.

XX

XX

PD 18-OCT-2001.

XX

XX

PF 09-APR-2001; 2001WO-US10802.

XX

XX

PR 07-APR-2000; 2000US-195225P.

XX

XX

PA (ZHAN/) ZHANG H M.

PA (AXRL/) AX R L.

XX

XX

PI Zhang HM, Ax RL;

XX

XX

DR WPI; 2002-066307/09.

DR P-PSDB; AAU11517.

XX

XX

PT Novel human or bovine fertility-associated antigen useful for

PT stabilising sperm cell acrosome and increasing fertility of a male

XX

PS Claim 1; Fig 2A-E; 54pp; English.

XX

XX

CC The invention describes a novel isolated human fertility-associated

CC antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful

CC for increasing the stability of a sperm cell acrosome and for increasing

CC the fertility of a human male by administering FAA. Detecting single

CC nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful

CC for assaying fertility by detecting the presence or absence of a FAA SNP

CC in the mammal and correlating the presence or absence with the fertility

CC of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the

CC specification. FAA SNP is also useful for determining the reproductive

CC fitness of a human or bovine, by determining the nucleotide sequence of

CC the FAA SNP, quantifying the fertility of more than one mammal containing

CC the FAA SNP and correlating the frequency of the FAA SNP to the

CC reproductive fitness of the mammals. FAA improves the integrity of sperm

CC membranes and increases the capacitation of sperm derived from either

CC fertile or infertile humans. Early genetic identification of infertility

CC improves the prognosis for subsequent attempts at fertilisation and

CC facilitates early intervention to determine whether the individual may

CC benefit from fertility treatments to avoid costly and/or emotional

CC problems with attempted inseminations. This sequence encodes the human

CC fertility-associated antigen (FAA), HCl, one of 4 partial prostate cDNA

CC clones of the novel FAA gene described in the method of the invention.

XX

SQ Sequence 556 BP; 159 A; 130 C; 142 G; 125 T; 0 other;

Query Match 83.2%; Score 492.4; DB 24; Length 556;

Best Local Similarity 96.0%; Pred. No. 3e-146;

Matches 505; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GAGAAGCTAAACGGAATTCAGAGAAAGGCATACATACAACTATGTGATTAGCTCTCGC 60

Db 31 GAGAAGCTGAACAGAAATTCAGAGAGAGGCATACGTCACAACTATGTGATTAGCTCTCGG 90

QY 61 CTTGGAAGAAACATATATAAAGAACAGTAGTCCTTTCTTATAAAGAAAAGCTAGTGCT 120

Db 91 CTTGGAAGAAACATATATAAAGAACAAATATGCTTTCTCTACAAGGAAAAGCTGGTGCT 150

QY 121 GTAAACAAAGCTACCTCTACCAAGCAGTATCAGGCTGGAGACGAGATGTGTTTCCAGG 180

Db 151 GTGAAGAGGAGTTATCACTACCATGACTATCAGGATGGAGACGAGATGTGTTTCCAGG 210

QY 181 GAACCCCTTTGCTGTGTTCCAGTCAACCCCTACACCGCTGTCAAGGACTTCGTGATTGTC 240

Db 211 GAACCCCTTTGCTGTGTTCCAGTCAACCCCTACACCGCTGTCAAGGACTTCGTGATTGTC 270

QY 241 CCCTGACACACCCCTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGATGCTAC 300

Db 271 CCCTGACACACCCCTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGATGCTAC 330

QY 301 ACAGATGTGAACGTCGCTCGAATGAGAGAAATTCATTTTCATGCTGGTGAATGCT 360

Db 331 ACAGATGTGAACGTCGCTCGAATGAGAGAAATTCATTTTCATGCTGGTGAATGCT 390

QY 361 GGCTGCAGCTACGTCCTCCCAAGAGGCTTGAAGAGACATCCGCTGAGGACGACCCCAAG 420

Db 391 GGCTGCAGCTACGTCCTCCCAAGAGGCTTGAAGAGACATCCGCTGAGGACGACCCCAAG 450

QY 421 TTCGTTGGCTGATCGGGACCAAGAGGACACCAACGGTCAAGAGAGACAAACTCGGCC 480

Db 451 TTCGTTGGCTGATCGGGACCAAGAGGACACCAACGGTCAAGAGAGACAAACTCGGCC 510

QY 481 TATCAGAGGATCGTCTTAGAGGACAAATATTTGTCAACTCTCGTG 526

Db 511 TATCAGAGGATCGTCTTAGAGGACAAATATTTGTCAACTCTCTTG 556

RESULT 5

ABN96895

ID ABN96895 standard; DNA; 1023 BP.

XX

AC ABN96895;

XX

DT 13-AUG-2002 (first entry)

XX

DE Gene #3393 used to diagnose liver cancer.

XX

KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;

KW metastatic liver tumour; cytostatic; expression profile; disease state;

KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX

OS Homo sapiens.

XX

PN WO200229103-A2.

XX

PD 11-APR-2002.

XX

PF 02-OCT-2001; 2001WO-US30589.

XX

PR 02-OCT-2000; 2000US-237054P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
XX determining a change in expression of a gene of a signature gene set
XX Claim 1; SEQ ID 251; 44pp; English.

XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.

XX Sequence 1023 BP; 312 A; 244 C; 240 G; 227 T; 0 other;

Query Match 80.5%; Score 476.8; DB 24; Length 1023;
Best Local Similarity 87.8%; Pred. No. 3.8e-141;
Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 GAGAGCTAAACGGAAATTAAGAAAGGCGATACATCAACTATGCTAGTCTCGC 60
DB 241 GAGAGCTGAACAGAAATTAAGAGAGGCGATACATCAACTATGCTAGTCTCGC 300
QY 61 CTGGAAGAAACACATATAAAGAACAGATGCTCTTCTATAAGAAAGCTAGTGTCT 120
DB 301 CTGGAAGAAACACATATAAAGAACATATGCTCTTCTATAAGAAAGCTAGTGTCT 360
QY 121 GTAAACAAAGCTACCTTACACAGCTATCAGGCTGAGAGCGAGATGTTTCCAGG 180
DB 361 GTGAAGAGGAGTTACTACATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 181 GAACCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 421 GAGCCCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 241 CCCCTGACACACCCCTGAGACATCCGTTTAGAGAGATGATGATGATGATGATGATGAT 300
DB 481 CCCCTGACACACCCCTGAGACATCCGTTTAGAGAGATGATGATGATGATGATGATGAT 540
QY 301 ACAGATGTAACGTCGCTGGAATGCAGAGATTTCAATTTTTCATGGTGAATCAATGCT 360
DB 541 ACGGACGTGAACACCCCTGGAAGCGGAGAAATTCATTTTTCATGGTGAATCAATGCT 600
QY 361 GGCTGACGTACGTCCTCCCAAGAGCCTGGAAGGACATCCGCTGAGGACGACCCCAAG 420
DB 601 GGCTGACGTACGTCCTCCCAAGAGCCTGGAAGGACATCCGCTGAGGACGACCCCAAG 660
QY 421 TTCGTTGGCTGATCGGGGACCAAGAGACACACGCTGGAAGAGAGACAAACTCGGCC 480
DB 661 TTTGTTGGCTGATCGGGGACCAAGAGACACACGCTGGAAGAGAGACCAACTCGGCC 720
QY 481 TATGACAGGATCGCTTATAGAGGACAAATATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 721 TATGACAGGATCGCTTATAGAGGACAAATATTCCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 541 CTCGCTTTTGTGATTTCCAGAAAGCTTACAGGTTGTCTGTAATCGAAGGCCCTGG 592
DB 781 AGTGTGTTTGTGATTTCCAGAAAGCTTACAGGTTGTCTGTAATCGAAGGCCCTGG 832

RESULT 7
ABL64458

ID ABL64458 standard; DNA; 1023 BP.
XX
AC ABL64458;
XX
DT 15-MAY-2002 (first entry)
XX
DE Stomach cancer related gene sequence SEQ ID NO:2795.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and

PT determining a change in expression of a gene of a signature gene set -
XX
PS Claim 1, SEQ ID 2795; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.
XX
SQ Sequence 1023 BP; 312 A; 244 C; 240 G; 227 T; 0 other;
Query Match 80.5%; Score 476.8; DB 24; Length 1023;
Best Local Similarity 87.8%; Pred. No. 3,8e-141;
Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 1 GAGACCTAAACCGAATTCAGAAAAGGCAATACATACATCTGTGATTAGCTCCG 60
DB 241 GAGAACTGACAGAAATTTAAGAGAGGCAATACATACATCTGTGATTAGCTCCG 300
QY 61 CTGGAAGAAACACATTAAGAAACAGTATGCTTTCTCTATTAAGAAAGCTAGTCT 120
DB 301 CTGGAAGAAACACATTAAGAAACATATGCTTTCTCTACAGAAAGCTGCTGCT 360
QY 121 GTAAAAAAGGACTCTTACACAGACTATCAGCTGAGACGCAATGTGTTCCAGG 180
DB 361 GTGAAGAGGAGTATCATCTACATGACTATCAGATGAGACGCAATGTGTTCCAGG 420
QY 181 GAACCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 421 GAACCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 241 CCCCTGACACCAACCCCTGAGATCCGTTAGAGATGATGAGTGTGTGTGTGTGTGT 300
DB 481 CCCCTGACACCAACCCCTGAGATCCGTTAGAGATGATGAGTGTGTGTGTGTGT 540
QY 301 ACAGATGTGAAGCGTCTGAGATGAGATTTCTTTTCAATGGTGAATTCATGCT 360
DB 541 ACAGATGTGAAGCGTCTGAGATGAGATTTCTTTTCAATGGTGAATTCATGCT 600
QY 361 GGTGAGAGTACGCTCCCAAGAGGCTGAGAGACATCCGCTGAGAGACGACCCCAAG 420
DB 601 GGTGAGAGTACGCTCCCAAGAGGCTGAGAGACATCCGCTGAGAGACGACCCCAAG 660
QY 421 TTGCTTGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 661 TTGCTTGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 481 TATGACAGATCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 721 TATGACAGATCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 541 CTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGATGAGAGGCTCTGG 592
DB 781 AGTGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGATGAGAGGCTCTGG 832
RESULT 8
ABL64961
ID ABL64961 standard; DNA; 1023 BP.
XX

AC ABL64961;
XX
DT 15-MAY-2002 (First entry)
XX
DE Lung cancer related gene sequence SEQ ID NO:3298.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
XX gene; de.
XX
OS Homo sapiens.
XX
PN W0200194629-A2.
XX
PD 13-DEC-2001.
XX
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236812P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX

PS Claim 1; SEQ ID 3298; 44pp; English.

XX The present invention describes a method (M1) for screening for an

CC anti-neoplastic agent. The method involves exposing cells to a chemical

CC agent to be tested for anti-neoplastic activity, determining a change in

CC expression of at least one gene (I) of a signature gene set, where (I)

CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664

CC to ABL70110), or is at least 95% identical to (S), where a change in

CC expression is indicative of anti-neoplastic activity. (I) has cytostatic

CC activity and can be used in gene therapy. M1 can be used for screening

CC an anti-neoplastic agent, and can be used for producing a product which

CC is the data collected with respect to the anti-neoplastic agent as a

CC result of M1, and the data is sufficient to convey the chemical

CC structure and/or properties of the agent. M1 can be used in the

CC treatment of cancer such as colon, breast, stomach, lung, thyroid,

CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,

CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,

CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine

CC carcinoma, papillary carcinoma and Wilms' tumour.

XX

XX Sequence 1023 BP; 312 A; 244 C; 240 G; 227 T; 0 other;

XX

Query Match 80.5%; Score 476.8; DB 24; Length 1023;

Best Local Similarity 87.8%; Pred. No. 3.8e-141;

Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 GAGAGCTAAACGGAAATTCAGAAAGGCGATACATCAACTATGTGATTAGCTCTCGC 60

DB 241 GAGAGCTGAACAGAAATTCAGGAGAGGCGATACGTCACACTATGTGATTAGCTCTCGG 300

QY 61 CTGGAAGAACACATATAAGAACAGATATGCTTTCTCTATAAGAAAGCTAGTGTCT 120

DB 301 CTGGAAGAACACATATAAGAACAAATATGCTTTCTCTACAGGAAAGCTGTGTCT 360

QY 121 GTAAACAAAGCTACTCTACACAGCTATCAGGCTGAGAGCGAGATGTGTTTCCAGG 180

DB 361 GTGAGAGAGATTATCACTACATGACTATCAGGATGAGAGCGAGATGTGTTTCCAGG 420

QY 181 GAACCCCTTTGGTGTGTTCCAGTCACTCCCTACACCGCTGTCAAGGACTTCGTGATTGTC 240

DB 421 GAGCCCTTTGGTGTGTTCCAAATCTCCACACTGCTGTCAAGAGCTTCGTGATTATC 480

QY 241 CCCCTGCACACCCCTCAGACATCCCTTAGAGAGATTGATGAGCTGGCTGATGCTTAC 300

DB 481 CCCCTGCACACCCCTCAGACATCCCTTAAGGAGATCGATGAGTTGGTTGAGGCTTAC 540

QY 301 ACAGATGTGAACCGTCTGGAATGCAGAGAAATTTCAATTTTCATGGGTGACTTCAATGCT 360

DB 541 ACGGACGTGAACACCGCTGGAAGCGGAGAAATTTCAATTTTCATGGGTGACTTCAATGCC 600

QY 361 GGCTGCAGCTACGTCCTCCCAAGAGCGCTGGAAGGACATCCGCTTAGAGACCGGACCCCAAG 420

DB 601 GGCTGCAGCTACGTCCTCCCAAGAGCGCTGGAAGAACATCCGCTTAGAGACTGACCCCAAG 660

QY 421 TTCCTTGGCTGATCGGGGACCAAGAGACACCCAGCTCAAGAGAGACACAACTGCGCC 480

DB 661 TTTGTTGGCTGATCGGGGACCAAGAGACACCCAGCTGGAAGAGAGACCAACTGTGCA 720

QY 481 TATGACGATGCTGCTTAGAGGACAAATATTTGCAACTCTGGTGGTCTCAATCAAAAC 540

DB 721 TATGACGATGCTGCTTAGAGGACAAAGAAATCGTCAGTTCTGTTTCCCAAGTCAAAAC 780

QY 541 CTCGCTTTGATTTCAGAAAGCTTACAGGTTGCTGAAATCGAAGGCCCTCG 592

DB 781 AGTGTGTTTGTGCTCCAGAAAGCTTACAAAGCTGACTGAAGAGGAGGCCCTCG 832

RESULT 9

AAT74076

ID AAT74076 standard; cDNA; 1079 BP.

XX

AC AAT74076;

XX

DT 29-JAN-1998 (first entry)

XX Human LS-DNase nucleotide sequence.

DE

XX DNase; actin; DNA viscoelasticity; systemic lupus erythematosus;

XX cystic fibrosis; meningitis; pulmonary disease; gene therapy;

KW recombinant preparation; DNA hydrolytic activity; ss.

KW

XX Homo sapiens.

OS

XX Key Location/Qualifiers

PH 71..988

FT CDS

FT sig_peptide /tag= a

FT mat_peptide /tag= b

FT /tag= c

FT /product= LS-DNase

XX

PN WO9728266-A1.

XX

XX 07-AUG-1997.

XX

XX 03-FEB-1997; 97WO-US01506.

XX

XX 05-FEB-1996; 96US-0597078.

PR

XX (GETH) GENENTECH INC.

XX

XX Baker KP, Baron WF;

PI

XX WPI; 1997-402619/37.

DR

XX P-PSDB; AAW23542.

XX

XX New isolated LS-DNase which is resistant to inhibition by actin -

PT used for the treatment of e.g systemic lupus erythematosus and

PT pulmonary diseases and disorders such as cystic fibrosis

XX

XX Claim 1; Fig 1; 32pp; English.

XX

XX This DNA sequence encodes a novel human LS-DNase (AAW23542), which has

CC DNA-hydrolytic activity but is resistant to inhibition by actin. It can

CC be used for reducing the viscoelasticity or viscous consistency of

CC DNA-containing material, as well as treatment of systemic lupus

CC erythematosus or pulmonary disease of disorders such as cystic fibrosis,

CC bronchitis, pneumonia, bronchiectasis, emphysema, asthma, tuberculosis

CC or fungal infections. It can also be used for adjunctive treatment of

CC abscesses or severe closed-space infections in conditions such as

CC empyema, meningitis, peritonitis, sinusitis, otitis, periodontitis,

CC pericarditis, pancreatitis, cholelithiasis, endocarditis and

CC septic arthritis, as well as in topical treatments in a variety of

CC inflammatory and infected lesions, e.g. of the skin and mucosal

CC membranes, surgical wounds, ulcerative lesions and burns. LS-DNase may

CC improve the efficacy of antibiotics used in the treatment of such

CC infections (e.g. gentamicin activity is markedly reduced by reversible

CC binding to intact DNA). It can also be used for the treatment of other

CC non-infected conditions in which there is an accumulation of cellular

CC debris that includes cellular DNA, such as pyelonephritis and

CC tubulo-interstitial kidney disease. It can also be used in vitro

CC diagnostic assays of a viscous material (e.g. sputum) from a patient.

CC The anti-LS-DNase antibodies can be used for detection and purification

CC of LS-DNase.

XX

XX Sequence 1079 BP; 330 A; 260 C; 252 G; 237 T; 0 other;

XX

Query Match 80.5%; Score 476.8; DB 18; Length 1079;

Best Local Similarity 87.8%; Pred. No. 3.9e-141;

Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 GAGAGCTAAACGGAAATTCAGAAAGGCGATACATCAACTATGTGATTAGCTCTCGC 60

DB 287 GAGAGCTGAACAGAAATTCAGGAGAGGCGATACACATGATGTGATTAGCTCTCGG 346

QY 61 CTTGGAAGAAACATATTAAGAAACAGTAGCCCTTTCTCTATTAAGAAACCTAGTGTCT 120
 DB 347 CTTGGAAGAAACATATTAAGAAACATATGCTTTCTCTACAGAAAGAAAGCTGTGTCT 406
 QY 121 GTAAACAAAGCTACCTCTACAGACTATACAGCTGAGACGAGATGTGTCTTCCAGG 180
 DB 407 GTGAAGAGAGATTATCACTACCATGACTATCAGATGAGAGCGAGATGTGTCTCCAGG 466
 QY 181 GAACCCCTTTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 467 GAGCCCTTTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
 QY 241 CCCCTGACACACCCCTGAGACATCCGTTAGAGATTTGATGAGCTGCTGATGTCTAC 300
 DB 527 CCCCTGACACACCCCTGAGACATCCGTTAGAGATTTGATGAGCTGCTGATGTCTAC 586
 QY 301 ACAGATGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 587 ACAGATGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
 QY 361 GGCCTGACGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 647 GGCCTGACGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
 QY 421 TTGCTTTGGCTGATCGGAGACCAAGAGACACACGCTCAAGAAAGACCAACTGCGCC 480
 DB 707 TTGCTTTGGCTGATCGGAGACCAAGAGACACACGCTCAAGAAAGACCAACTGCGCA 766
 QY 481 TATGACAGGATCGCTGCTTATAGAGCAAAATTTGTCAACTGTGTGTCTCAATCAAC 540
 DB 767 TATGACAGGATCGCTGCTTATAGAGCAAAATTTGTCAACTGTGTGTCTCAATCAAC 826
 QY 541 CTGCTCTTTGATTTCCAGAAAGCTTACAGGTTCTGATGATGAGGCGCTGG 592
 DB 827 AGCTTTTTCCTTCCAGAAAGCTTACAGGTTCTGATGATGAGGCGCTGG 878

RESULT 10

ABK84429 standard; cDNA; 1108 BP.

ABK84429;

14-AUG-2002 (first entry)

DE Human cDNA differentially expressed in granulocytic cells #1000.
 XX
 XX
 XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KM viral infection; parasitic infection; protozoal infection;
 KM fungal infection; sterile inflammatory disease; psoriasis;
 KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KM cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KM adult respiratory distress syndrome; inflammatory bowel disease;
 KM Crohn's disease; ulcerative colitis; peridontal disease;
 KM granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200228999-A2.
 PD 11-APR-2002.
 PF 03-OCT-2001; 2001WO-US30821.
 PR 03-OCT-2000; 2000US-237189P.
 XX (GENE-) GENE LOGIC INC.
 XX
 PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 DR WPI, 2002-435328/46.
 XX
 PT Detecting granulocyte activation by detecting differential expression

PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity

PS Claim 1; SEQ ID No 1000; 114bp; English.

XX
 XX The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC peridontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 1108 BP; 329 A; 261 C; 271 G; 247 T; 0 other;

CC Query Match 80.3%; Score 475.2; DB 24; Length 1108;

CC Best Local Similarity 87.7%; Pred. No. 1,3e-140;

CC Matches 519; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 GAGAGCTAAACGGAATTAAGAAAGCATATACATATGATGATGCTCCG 60
 DB 309 GAGAGCTAAACGGAATTAAGAAAGCATATACATATGATGATGCTCCG 368
 QY 61 CTTGGAAGAAACATATTAAGAAAGCATATGCTTTCTCTATTAAGAAAGCTAGTGTCT 120
 DB 369 CTTGGAAGAAACATATTAAGAAAGCATATGCTTTCTCTACAGAAAGCTGTGTCT 428
 QY 121 GTAAACAAAGCTACCTCTACAGACTATACAGCTGAGACCGAGATGTGTCTCCAGG 180
 DB 429 GTGAAGAGAGATTATCACTACCATGACTATCAGATGAGAGACGAGATGTGTCTCCAGG 488
 QY 181 GAACCCCTTTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 489 GAGCCCTTTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
 QY 241 CCCCTGACACACCCCTGAGACATCCGTTAGAGATTTGATGAGCTGCTGATGTCTAC 300
 DB 549 CCCCTGACACACCCCTGAGACATCCGTTAGAGATTTGATGAGCTGCTGATGTCTAC 608
 QY 301 ACAGATGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 609 ACAGATGTGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668

QY 361 GGCTGAGCTACGTCCTCCCAAGAGCCCTGGAGGACATCCGCTTGAGGACGAGCCCAAG 420
Db 669 GGCTGAGCTACGTCCTCCCAAGAGCCCTGGAGGACATCCGCTTGAGGACGAGCCCAAG 728
QY 421 TTCGTTTGGCTGATCGGGGACCAAGAGGACACACCGGTCAAGAGAGACAAAACCTGGCC 480
Db 729 TTTGTTTGGCTGATCGGGGACCAAGAGGACACACCGGTGAAGAGAGACCAACACTGTGCA 788
QY 481 TATGACAGGATCGTCTTAGAGGACAAATATTGTCAACTCTGGTGGTCTCAATCAAC 540
Db 789 TATGACAGGATGTGCTTAGAGGACAAATATCGTAGTTCTGTGTGTTCCCAAGTCAAC 848
QY 541 CTCGCTTTGATTCCAGAAAGCTTACAGGTTGCTGAATCGAAGGCGCTGG 592
Db 849 AGTGTGTTTGATCTCCAGAAAGCTTACAAGCTGACTGAAGAGGAGGCGCTGG 900

RESULT 11

AAT17733
ID AAT17733 standard; cDNA; 1208 BP.

XX AC AAT17733;

XX 17-OCT-1996 (first entry)

XX Deoxyribonuclease, DNase-gamma cDNA.

XX Deoxyribonuclease; DNase-gamma; selective cleavage; linker;
KW chromatin DNA; cell nucleus; 3'-hydroxy; 5'-phosphate; apoptosis;
KW carcinogenesis; AIDS development; diagnosis; prevention;
KW treatment; cancer; autoimmune disease; viral infections; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 12..944

XX /*tag= a

XX /note= "GAT codon comprising bases 837-839 has
no corresponding amino acid in AAR94021"

XX WO9607735-A1.

XX 14-MAR-1996.

XX 06-SEP-1995; 95WO-JP01775.

XX 06-SEP-1994; 94JP-0239518.

XX (TANU/) TANUMA S.

XX Tanuma S;

XX WPI; 1996-171610/17.

XX P-PSDB; AAR94021.

XX DNase which selectively cuts linker region of chromatin DNA -
PT useful in diagnosis, treatment and prevention of cancer, autoimmune
PT diseases, viral infections, etc.

XX Claim 4; Pages 55-57; 75pp; Japanese.

XX The present sequence encodes the deoxyribonuclease, DNase-gamma,
CC which is able to selectively cleave the linker part of chromatin
CC DNA. DNase-gamma has a mol. wt. of 32000 by SDS-PAGE, or 30000 by
CC gel filtration, an optimum pH of 5.6, is found in the cell nucleus,
CC is not dependent on divalent cations, has a Zn(2+) inhibition
CC IC(50) > 1mM and leaves 3'-OH and 5'-P termini after cleavage. The
CC DNase can be used at a mol. level to resolve the control
CC mechanisms of carcinogenesis, the autoimmune system and AIDS
CC development. It can also be used in the diagnosis, prevention and
CC treatment of cancer, autoimmune disease, viral infections, etc.,
CC and as an apoptosis control agent.

SQ Sequence 1208 BP; 319 A; 304 C; 282 G; 303 T; 0 other;

Query Match 76.2%; Score 451.2; DB 17; Length 1208;

Best Local Similarity 85.1%; Pred. No. 5.8e-133;

Matches 504; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1 GAGAAGCTAAACCGAAATTCAAGAAAGGCATAACATACAACTATGTAGTCTCTCGC 60

Db 243 GAGAAGCTGAATGGAAGCTCAGGAAGACGACATACAACTACGTGATAGTCTCTCGG 302

QY 61 CTTGGAAGAAACATATAAAGAACAGTATGCTCTTCTATAAAGAAAGCTAGTGTCT 120

Db 303 CTTGGAAGAAACATATAAAGAACAGTATGCTCTTCTTACAAGGAGAGCTGTGTCT 362

QY 121 GTAAACAAAGCTACCTCTACACGACTATCAGGCTGGAGACGAGATGTGTTTCCAGG 180

Db 363 GTGAAGGCAAAATACCTCTACCATGACTATCAGGATGGAGACACAGACGCTGTTTCCAGG 422

QY 181 GAACCCCTTTGTGTCTGGTTCCAGTCACCTACACGCTCTCAAGGACTTTCGTGATTGTC 240

Db 423 GAGCCCTTTGTGTGTTTCCAGGCGCCCTTCACTGCTCCCAAGGACTTTCGTGATTGTC 482

QY 241 CCCCTGCACACCCCTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGATGTCTAC 300

Db 483 CCCTTGCACACAACTCTGTAACCTCTGTTTAAAGAGATAGATGAGCTGGCTGACGTCTAC 542

QY 301 ACAGATGTGAACGCTGCTCGAATGAGAGAAATTTCAATTTTCTGATGCTCAATGCT 360

Db 543 ACGGATGTTAGAAGACGATGGAAGGACAGATTTTCACTTTCATGGTGATTTCAATGCT 602

QY 361 GGCTGCAGCTACCTCCCAAGAGGCTGGAAGGACATCCGCTGAGGAGGAGCCCAAG 420

Db 603 GGCTGCAGCTACCTCCCAAGAGGCTGGAAGGACATCCGCTTGAAGGAGGAGCCCAAG 662

QY 421 TTCGTTTGGCTGATCGGGGACCAAGAGGACACCAAGCTCAAGAGAGACAAACTGCGCC 480

Db 663 TTTGTTTGGCTGATCGGGGACCAAGAGGACACCAAGCTCAAGAGAGACCAAGCTGTCG 722

QY 481 TATGACAGGATCGTGCTTAGAGGACAAATATTTGTCACCTCTGGTGCTCTCAATCAAC 540

Db 723 TATGACAGGATTCGTGTTCCGGGACCAAGAGATAGTCAACTCTGTGTGTTCCCGCTCCAGT 782

QY 541 CTGCTCTTTCGATTCCAGAAAGCTTACAGGTTGCTCAATCGAAGGCGCTGG 592

Db 783 GCGCTCTTTCGACTTTCAGAAAGCTTATGAGTTGTCTGAAGAGGAGGCGCTGG 834

RESULT 12

AAT74083

ID AAT74083 standard; cDNA; 1124 BP.

XX AC AAT74083;

XX 29-JAN-1998 (first entry)

XX Murine LS-DNase nucleotide sequence.

XX DNase; actin; DNA viscoelasticity; systemic lupus erythematosus;
KW cystic fibrosis; meningitis; pulmonary disease; gene therapy;
KW recombinant preparation; DNA-hydrolytic activity; ss.

XX Mus sp.

XX Key Location/Qualifiers

XX CDS 173..1105

XX /*tag= a

XX sig_peptide 173..247

XX /*tag= b

XX /note= "putative"

XX mat_peptide 248..1105

XX /*tag= c

XX /product= LS-DNase

PN W09728266-A1.
 XX 07-AUG-1997.
 PD
 XX
 PF 03-FEB-1997; 97MO-US01506.
 XX
 PR 05-FEB-1996; 96US-0597078.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Baron WF;
 PI
 XX WPI; 1997-402619/37.
 DR
 XX
 PT New isolated LS-DNase which is resistant to inhibition by actin -
 PT used for the treatment of e.g systemic lupus erythematosus and
 PT pulmonary diseases and disorders such as cystic fibrosis
 PS
 XX Example 6; Fig 3; 32pp; English.

CC This DNA sequence encodes a variant LS-DNase, which has DNA-hydrolytic
 CC activity but is resistant to inhibition by actin. A 649 base pair
 CC fragment of the coding sequence of cloned human LS-DNase (AAT74076) was
 CC used to screen a murine liver cDNA library and obtain this nucleotide.
 CC Murine mature LS-DNase is 84% identical to human LS-DNase. A portion of
 CC the present sequence was used in Northern blot assays of various murine
 CC tissues. Expression of murine LS-DNase mRNA was found to be highest in
 CC the liver and spleen. Human LS-DNase can be used for reducing the
 CC viscoelasticity or viscous consistency of DNA-containing material, as
 CC well as treatment of systemic lupus erythematosus or pulmonary disease
 CC disorders such as cystic fibrosis. It can also be used for adjunctive
 CC treatment of abscesses or severe closed-space infections, e.g.
 CC meningitis. It may improve the efficacy of antibiotics used in the
 CC treatment of such infections (e.g. gentamicin activity is markedly
 CC reduced by reversible binding to intact DNA). It can also be used in in
 CC vitro diagnostic assays of a viscous material (e.g. sputum) from a
 CC patient. The anti-LS-DNase antibodies can be used for detection and
 CC purification of LS-DNase.

SQ Sequence 1124 BP; 299 A; 273 C; 273 G; 279 T; 0 other;

Query Match 73.5%; Score 435.2; DB 18; Length 1124;
 Best Local Similarity 83.4%; Pred. No. 6.9e-128;
 Matches 494; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 GAGAGCTAAACGGAATTCAGAAAAGCATACATATGATGATTAGCTTCGC 60
 DB 404 GAGAGCTGAATGAAATTCAGAAAGACACAACTATGATGATTAGCTTCGA 463
 QY 61 CTGGAAGAAACATATTAAGAACAGTATGCTTCTCTATTAAGAAAGCTAGTGTCT 120
 DB 464 CTGGAAGAAACATATTAAGAACAGTATGCTTCTCTATTAAGAAAGCTAGTGTCT 523
 QY 121 GTAAAAAAGGACTCTCTATCAAGACTATCAGGCTGAGACGAGATGTTTCCAGG 180
 DB 524 GTAAAGCAAAATATCACTACATGATCAGATGAGACAGACGATTTCCAGG 583
 QY 181 GAACCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 DB 584 GAACCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 643
 QY 241 CCCTGACACCAACCCCTGAGACATCGTTAGAGATTGATGAGGCTGATGATGTAC 300
 DB 644 CCCTGACACCAACCCCTGAGACATCGTTAGAGATTGATGAGGCTGATGATGTAC 703
 QY 301 ACAGATGTGAAGCGTCTGGAATGACAGAAATTTCTTTCATGAGGCTCAATGCT 360
 DB 704 ACAGATGTGAAGCGTCTGGAATGACAGAAATTTCTTTCATGAGGCTCAATGCT 763
 QY 361 GGTTCAGAGTACGTTCCCAAGAGGCTTGAAGACATCGCTGAGAGAGGACCCCAAG 420
 DB 764 GGTTCAGAGTACGTTCCCAAGAGGCTTGAAGACATCGCTGAGAGAGGACCCCAAG 823

QY 421 TTGCTTTGGCTGATCGGGGACCAAGAGACACGCTCAAGAAGACAAACTGCGCC 480
 DB 824 TTGCTTTGGCTGATCGGGGACCAAGAGACACGCTCAAGAAGACATCAGCTGCGC 883
 QY 481 TATGACAGATTCGTGCTTGAAGACAAATATTTGTCACTCTGTGTCTCAATCAAC 540
 DB 884 TATGACAGATTCGTGCTTGAAGACAAAGATGATCACTCCGTGTCTCCCGTTCAGT 943
 QY 541 CTGCTTTGATTTCCGAAGCTTACAGTGTCTGATTCGAAGGCGCTGG 592
 DB 944 GCGCTTTGATTTCCGAAGCTTACAGTGTCTGATTCGAAGGCGCTGG 995

RESULT 13

AAS17902
 ID AAS17902 standard; cDNA; 350 BP.
 XX
 AC AAS17902;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE partial cDNA encoding human fertility-associated antigen (FAA), HC2.
 XX
 KW Fertility-associated antigen; FAA; antifertility; sperm cell acrosome;
 KW reproductive fitness; single nucleotide polymorphism; SNP; human;
 KW HC2; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..349
 FT /tag= a
 FT /product= "Human FAA"
 FT /note= "Human fertility-associated antigen, HC2"
 FT /partial
 FT /note= "No start or stop codon given"
 XX
 PN W0200176529-A2.
 PD 18-OCT-2001.
 XX
 PF 09-APR-2001; 2001MO-US10802.
 XX
 PR 07-APR-2000; 2000US-195225P.
 XX
 PA (ZHAN/) ZHANG H M.
 PA (AXRL/) AX R L.
 XX
 PI Zhang HM, Ax RL;
 XX
 DR WPI; 2002-066307/09.
 DR P-PSDB; AAU11518.
 XX
 PT Novel human or bovine fertility-associated antigen useful for
 PT stabilizing sperm cell acrosome and increasing fertility of a male
 PS Claim 1; Fig 2A-E; 54pp; English.
 XX
 CC The invention describes a novel isolated human fertility-associated
 CC antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful
 CC for increasing the stability of a sperm cell acrosome and for increasing
 CC the fertility of a human male by administering FAA. Detecting single
 CC nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful
 CC for assaying fertility by detecting the presence or absence of a FAA SNP
 CC in the mammal and correlating the presence or absence with the fertility
 CC of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the
 CC specification. FAA SNP is also useful for determining the reproductive
 CC fitness of a human or bovine, by determining the nucleotide sequence of
 CC the FAA SNP, quantifying the fertility of more than one mammal containing
 CC the FAA SNP and correlating the frequency of the FAA SNP to the
 CC reproductive fitness of the mammals. FAA improves the integrity of sperm
 CC membranes and increases the capacitation of sperm derived from either
 CC fertile or infertile humans. Early genetic identification of infertility

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2002, 09:20:03 ; Search time 1320.4 Seconds
(without alignments)
7261.235 Million cell updates/sec

Title: US-09-905-114-1
Perfect score: 592
Sequence: 1 ggaagctaaacggaatc.....gctgaatcgaagccctcg 592

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
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8: em_hic:*
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16: em_estom:*
17: gb_gse:*
18: em_gse_hum:*
19: em_gse_inv:*
20: em_gse_pin:*
21: em_gse_vrt:*
22: em_gse_fun:*
23: em_gse_mam:*
24: em_gse_mus:*
25: em_gse_other:*
26: em_gse_pro:*
27: em_gse_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	478.4	80.8	890	9	AL546857 AL546857
2	476.8	80.5	896	9	AL546432 AL546432
3	471.8	79.7	833	9	AL572037 AL572037
4	469	79.2	931	9	AL571894 AL571894
5	438.8	74.1	506	10	AV607154 AV607154
6	432	73.0	666	10	BE048177 BE048177 tz46h09.y

C 7	421	71.1	695	13	BI522352	603081420
C 8	411.6	69.5	642	10	AM543356	CO168H07-
C 9	406	68.6	825	12	BC687772	BC687772
C 10	396.4	67.0	825	12	BC530136	BC530136
C 11	391.2	66.1	820	10	AM543802	AM543802
C 12	389.4	65.8	628	13	BI460950	BI460950
C 13	386	65.2	610	10	AM540389	AM540389
C 14	383.8	64.8	668	10	AM915564	AM915564
C 15	383.6	64.8	784	9	AI927844	AI927844
C 16	376	63.5	832	13	BI838188	BI838188
C 17	363.4	61.4	634	9	AI660448	AI660448
C 18	363.4	61.4	981	14	BO710632	BO710632
C 19	361	61.0	685	13	BI833952	BI833952
C 20	353.2	59.7	566	10	AM538998	AM538998
C 21	351	59.3	759	12	BC534290	BC534290
C 22	330.2	55.8	527	10	AM539589	AM539589
C 23	328.2	55.4	613	10	AM779563	AM779563
C 24	328	55.4	578	10	AM658627	AM658627
C 25	311	52.5	643	10	AM001760	AM001760
C 26	303.8	51.3	714	12	BC566893	BC566893
C 27	302.2	51.0	855	12	BF237166	BF237166
C 28	296.8	50.1	542	12	BF434855	BF434855
C 29	291.2	49.2	901	12	BF303508	BF303508
C 30	290	49.0	554	10	AM243180	AM243180
C 31	288.8	48.8	555	9	AI134430	AI134430
C 32	288.2	48.7	487	9	AI194886	AI194886
C 33	279.8	47.3	341	10	AM803005	AM803005
C 34	279.6	47.2	497	9	AA564572	AA564572
C 35	277.2	46.8	586	13	BM489658	BM489658
C 36	267.6	45.2	522	14	BO186387	BO186387
C 37	265.6	44.9	595	12	BC077563	BC077563
C 38	262.6	44.4	453	14	H78170	H78170
C 39	261.2	44.1	433	12	BF911384	BF911384
C 40	252.4	42.6	511	9	AI271665	AI271665
C 41	248.4	42.0	523	9	AI248904	AI248904
C 42	240.4	40.6	536	9	AA707043	AA707043
C 43	239.6	40.5	486	9	AA989198	AA989198
C 44	237.6	40.1	498	12	BC064211	BC064211
C 45	236.2	39.9	427	10	AM827162	AM827162

ALIGNMENTS

RESULT 1
LOCUS AL546857 890 bp mRNA linear EST 16-FEB-2001
DEFINITION AL546857 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1026YK08 5
ACCESSION AL546857
VERSION AL546857.1 GI:12880381
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/db_xref="taxon:9606"
/clone="CSOD1026YK08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="Placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/

BASE COUNT 250 a 215 c 220 g 204 t 1 others

Query Match	80.8%;	Score 478.4;	DB 9;	Length 890;
Best Local Similarity	88.0%;	Pred. No. 1.1e-128;		
Matches 521;	Conservative 0;	Mismatches 71;	Indels 0;	Gaps 0;

QY	1	GAGAAAGCTAAACGGAAATTCAGAGAAAGGCAATACATACATCTATGTGATTAGCTCTCGC	60
Db	216	GAGAAAGCTGAACAGAAATTCAGAGAGAGGCAATACATACATCTATGTGATTAGCTCTCGG	275
QY	61	CTTGGAGAAACACATATAAAGACAGATATGCTTTCTCTATAAGAAAGCTAGTGTCT	120
Db	276	CTTGGAGAAACACATATAAAGAAATATGCTTTCTCTACAGAGAAAGCTGGTGTCT	335
QY	121	GTAAACAAAGCTACCTCTACACAGCTATCAGCTGGAGAGCAGATGTGTTTCCAGG	180
Db	336	GTGAAGAGGAGTTATCACTACCATGACTATCAGATGGAGAGCAGATGTGTTTCCAGG	395
QY	181	GAACCTTTGTGGTCTGCTTCCAGTCACTACACCGCTGTCAAGGACTTCGTTGATGTCT	240
Db	396	GAGCCCTTTGTGGTCTGCTTCCATCTCCACACTGCTGTCAAGACTTCGTTGATGTCT	455
QY	241	CCCTGTCACACACCCCTGAGACATCCGTTAGAGAGATGTAGCTGGCTGATGTCTAC	300
Db	456	CCCTGTCACACACCCCTGAGACATCCGTTAAGGAGATCGATGATGTGTTGAGGTCTAC	515
QY	301	ACAGATGTGAACGTCGCTGGAATTCAGAGAAATTTCAATTTTCATGGGTGACTTCAATGCT	360
Db	516	ACGGACGTGAACACACCGCTGGAGGCGGAGAAATTTCAATTTTCATGGGTGACTTCAATGCC	575
QY	361	GGCTCAGCTACGTCCTCCCAAGAGCCCTGGAAGGACATCCGCTGAGAGACCCCAAG	420
Db	576	GGCTCAGCTACGTCCTCCCAAGAGCCCTGGAAGAAATCCGCTTGAGGACTGACCCCAAG	635
QY	421	TTGCTTTGGCTGATCGGGACCAAGAGACACCGTTCAGAGAGACACAACTGGCC	480
Db	636	TTTGTGTTGGCTGATCGGGACCAAGAGACACCGTGAAGAGAGACCAACTGTGCA	695
QY	481	TATGACAGGATCGCTTAGAGGACAAATATTTGTCATCTGGTGGTCAATCAATCAAC	540
Db	696	TATGACAGGATTTGCTTAGAGGACAAAGAAATCGTCAGTTCTGTTGTTCCCAAGTCAAC	755
QY	541	CTCGCTTTGATTTCAGAAAGCTTACAGGTTGTCTGAATCAAGGCGCTCGG	592
Db	756	AGTGTGTTTGGACTTCCAGAAAGCTTACAGCTGACTGAAGAGAGGCGCTCGG	807

RESULT 2
AL546432 896 bp mRNA linear EST 16-FEB-2001
LOCUS AL546432 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI030YD20 5
DEFINITION prime, mRNA sequence.
ACCESSION AL546432
VERSION AL546432.1 GI:12879540
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 896)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .896
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI030YD20"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site: 1. NotI; let strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/

BASE COUNT 249 a 217 c 226 g 203 t 1 others

Query Match	80.5%;	Score 476.8;	DB 9;	Length 896;
Best Local Similarity	87.8%;	Pred. No. 3.1e-128;		
Matches 520;	Conservative 0;	Mismatches 72;	Indels 0;	Gaps 0;

QY	1	GAGAAAGCTAAACGGAAATTCAGAGAAAGGCAATACATACATCTATGTGATTAGCTCTCGC	60
Db	266	GAGAAAGCTGAACAGAAATTCAGAGAGAGGCAATACATCTATGTGATTAGCTCTCGG	325
QY	61	CTTGGAGAAACACATATAAAGAAAGTATGCTTTCTCTATAAGAAAGCTAGTGTCT	120
Db	326	CTTGGAGAAACACATATAAAGAAATATGCTTTCTCTACAGAAAGCTGGTGTCT	385
QY	121	GTAAACAAAGCTACCTCTACACGACTATCAGGCTGGAGAGCAGATGTGTTTCCAGG	180
Db	386	GTGAAGAGGAGTTATCACTACCATGACTATCAGATGGAGAGCAGATGTGTTTCCAGG	445
QY	181	GAACCTTTGTGCTGCTGTTCCAGTCACTACACCGCTGTCAAGGACTTCGTTGATTGC	240
Db	446	GAGCCCTTTGTGCTGCTGTTCCAAATCTCCCACTGCTGTCAAGACTTCGTTGATTATC	505
QY	241	CCCTGTCACACACCCCTGAGACATCCGTTAGAGAGATGTAGCTGGCTGATGTCTAC	300
Db	506	CCCTGTCACACACCCCTCAGAGACATCCGTTAAGAGATCGATGTTGTTGAGGTCTAC	565
QY	301	ACAGATGTGAACGTCGCTGGAAATGAGAGAAATTTCAATTTTCATGGTGAATGCT	360
Db	566	ACGACGCTGAACACACCGCTGGAAGGCGGAGAAATTTCAATTTTCATGGTGAATGCT	625
QY	361	GGCTGACGCTACGTCCTCCCAAGAGGCTGGAAGGACATCCGCTGAGGACGACCCCAAG	420
Db	626	GGCTGACGCTACGTCCTCCCAAGAGGCTGGAAGAAATCCGCTTGAGGACTGACCCCAAG	685
QY	421	TTGCTTTGGCTGATCGGGACCAAGAGGACACCGCTCAAGAGAGACAAACTGCGCC	480
Db	686	TTTGTGTTGGCTGATCGGGACCAAGAGGACACCGCTGAAGAGAGACCAACTGTGCA	745
QY	481	TATGACAGGATCGCTTAGAGGACAAATATTTGTCATCTGGTGGTCTCAATCAATCAAC	540
Db	746	TATGACAGGATTTGCTTAGAGGACAAAGAAATCGTCAGTTCTGTTGTTCCCAAGTCAAC	805
QY	541	CTCGCTTTGATTTCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCGCTCGG	592
Db	806	AGTGTGTTTGGACTTCCAGAAAGCTTACAGCTGACTGAAGAGAGGCGCTCGG	857

RESULT 3
AL572037/c 833 bp mRNA linear EST 16-FEB-2001
LOCUS AL572037 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI026YK08 3
DEFINITION prime, mRNA sequence.

ACCESSION AL572037
VERSION AL572037.1 GI:12929919
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 833)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
FEATURES
source
1. 833
/organism="Homo sapiens"
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/clone_lib="LTI NFL006_PL2"
/issue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 193 a 193 c 191 g 249 t 7 others
ORIGIN
Query Match 79.7%; Score 471.8; DB 9; Length 833;
Best Local Similarity 87.0%; Pred. No. 8.7e-127;
Matches 515; Conservative 2; Mismatches 75; Indels 0; Gaps 0;

QY 1 GAGAACTAAACGGAATTCAGAAAGGCAATACATACATATGATAGCTCTCCG 60
DB 734 GAGAACTGAAAGAAATTCAGAAAGGCAATACATACATATGATAGCTCTCCG 675
QY 61 CTGGAAGAAACATATTAAGAAACATATGCTCTCTATTAAGAAAGCTAGTGTCT 120
DB 674 CTGGAAGAAACATATTAAGAAACATATGCTCTCTCTCAAGAAAGCTGCTCT 615
QY 121 GTAACCAAAAGCTACTCTACACAGACTATCAGGCTGAGAGCGGAGATGTTTCCAG 180
DB 614 GTGAAGAGGATTAATCACTACATGACTATCAGATGAGAAACGAGATGTTTCCAG 555
QY 181 GAACCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 554 GAACCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 495
QY 241 CCCCTGACACACCCCTGAGACATCGTTAGAGATGTTGAGCTGGGCTGATGTCTAC 300
DB 494 CCCCTGACACACCCCTGAGACATCGTTAGAGATGTTGAGCTGGGCTGATGTCTAC 435
QY 301 ACAGATGTGAAGCTCGCTGGAATGACAGAAATTTCTTTTCAATGCT 360
DB 434 ACAGAGGTGAAGACCGCTGGAAGGAGGAGATTTTCAATGCTGATCAATGCT 375
QY 361 GGTGTCAGCTACGTTCCCAAGAGGCTGAGAGACATCGCTGAGAGAGGAGAGG 420
DB 374 GGTGTCAGCTACGTTCCCAAGAGGCTGAGAGACATCGCTGAGAGAGGAGAGG 315
QY 421 TTGCTTTGGCTGATCGGGGCAAGAGAGACACCGCTCAAGAGAGACAAATGCGCC 480
DB 314 TTGCTTTGGCTGATCGGGGCAAGAGAGACACCGCTCAAGAGAGACAAATGCGCA 255
QY 481 TATGACAGATCGTGTAGAGGCAAAATATTTGCTCAACTCTGCTGCTCTCAATCAAC 540
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DB 254 TATGACAGATTTGCTTGAAGACAGAAATGCTGATTTGTTCCAGTCAAC 195
QY 541 CTCGCTTTGATTTCCAGAAAGCTTACAGTTGCTGAATTCAGAGCCCTGG 592
DB 194 AGCTTTTGTGACTTCCAGAAAGCTTACAGTGTGAGAGAGGAGGCTTGG 143
RESULT 4
AL571894/c 931 bp mRNA linear EST 16-FEB-2001
LOCUS AL571894 LTI_NFL006_PL2 Homo sapiens cDNA clone CSOD1030YD20 3
DEFINITION prime, mRNA sequence.
ACCESSION AL571894
VERSION AL571894.1 GI:12929641
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 931)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
FEATURES
source
1. 931
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/db_xref="taxon:9606"
/clone="CSOD1030YD20"
/clone_lib="LTI NFL006_PL2"
/issue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 209 a 219 c 225 g 271 t 7 others
ORIGIN
Query Match 79.2%; Score 469; DB 9; Length 931;
Best Local Similarity 86.8%; Pred. No. 6e-126;
Matches 514; Conservative 1; Mismatches 77; Indels 0; Gaps 0;

QY 1 GAGAACTAAACGGAATTCAGAAAGGCAATACATACATATGATAGCTCTCCG 60
DB 726 GAGAACTGAAAGAAATTCAGAAAGGCAATACATACATATGATAGCTCTCCG 667
QY 61 CTGGAAGAAACATATTAAGAAACATATGCTCTCTATTAAGAAAGCTAGTGTCT 120
DB 666 CTGGAAGAAACATATTAAGAAACATATGCTCTCTCTCAAGAAAGCTGCTCT 607
QY 121 GTAACCAAAAGCTACTCTACACAGACTATCAGGCTGAGAGCGGAGATGTTTCCAG 180
DB 666 CTGGAAGAAACATATTAAGAAACATATGCTCTCTCTCAAGAAAGCTGCTCT 607
QY 181 GAACCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 546 GAACCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 487
QY 241 CCCCTGACACACCCCTGAGACATCGTTAGAGATGTTGAGCTGGGCTGATGTCTAC 300
DB 486 CCCCTGACACACCCCTGAGACATCGTTAGAGATGTTGAGCTGGGCTGATGTCTAC 427
QY 301 ACAGATGTGAAGCTCGCTGGAATGACAGAAATTTCTTTTCAATGCT 360
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Db 426 ACGACGTGAACACCCGCTGAAGCGGAGAAATTTCAATTTTCATGGGTGACTTCAATGCC 367
QY 361 GGCTGCAGCTACGTCCTCCCAAGAGCCCTGGAAAGACATCCGCTTGAGGACGACCCCAAG 420
Db 366 GGCTGCAGCTACGTCCTCCCAAGAGCCCTGGAAAGACATCCGCTTGAGAACTGACCCCAAG 307
QY 421 TTCGTTTGGCTGATCGGGGACCAAGAGACACACCGGTGAAGAGAGACACAACTGGGCC 480
Db 306 TTTGTTTGGCTGATCGGGGACCAAGAGACACACCGGTGAAGAGAGACACCAACTGTCGA 247
QY 481 TATGACAGGATCGTCTTAGAGGACAAATATTCTCAACTCTGGTGTCTCAATCAAAAC 540
Db 246 TATAACAGGATGTGCTTAGAGGACAAATATTCTCAACTCTGGTGTCTCAATCAAAAC 187
QY 541 CTCGCTTTGATTTCCAGAAAGCTTACAGGTGTCTGAATCGAAGGCCCTGG 592
Db 186 AGTGTTTTGACTTCCAGAAAGCTTACAGCTGACTGAAGAGGAGGCCCTGG 135

RESULT 5
AV607154/c AV607154 506 bp mRNA linear EST 28-NOV-2001
LOCUS AV607154 Bos taurus kidney fetus Bos taurus cDNA clone E1KI039B05
DEFINITION 3', mRNA sequence.
ACCESSION AV607154
VERSION AV607154.1 GI:9737527
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 506)
AUTHORS Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
TITLE Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs
JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)
MEDLINE 21570554
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shrakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
FEATURES
source
1..506
/organism="Bos taurus"
/db_xref="taxon:9913"
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/lab_host="DH10B"
/notes="Vector: pZLI; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"
BASE COUNT 124 a 126 c 129 g 126 t 1 others
ORIGIN
Query Match 74.1%; Score 438.8; DB 10; Length 506;
Best Local Similarity 99.3%; Pred. No. 3.1e-117;
Matches 440; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 150 TAGGCTGAGACGCGAGATGCTTTTCAGGGACCCCTTGTGCTCGTCCAGTCACC 209
Db 506 TCAGGCTGAGACGCGAGATGCTTTTCAGGGACCCCTTGTGCTCGTCCAGTCACC 447
QY 210 CTACACCGCTGTCAAGGACTTCGTGATTTGTCCCTTCGACACCCCTTGAGACATCCGT 269
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Db 446 CTACACCGCTGTCAAGGACTTNGTGTGTCCTCCCTGCACACCCCTTGAGACATCCGT 387
QY 270 TAGAGAGATTGATAGCTGGCTGATGTCTACACAGATGTGAACGCTGCTGGAATGCAGA 329
Db 386 TAGAGAGATTGATAGCTGGCTGATGTCTACACAGATGTGAACGCTGCTGGAATGCAGA 327
QY 330 GAATTTCAATTTTCATGGGTGACTTCAATGCTGGCTGACGCTACGTCCTCCCAAGAGCCCTG 389
Db 326 GAATTTCAATTTTCATGGGTGACTTCAATGCTGGCTGACGCTACGTCCTCCCAAGAGCCCTG 267
QY 390 GAAGGACATCCGCTCGAGGACGAGCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGA 449
Db 266 GAAGGACATCCGCTCGAGGACGAGCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGA 207
QY 450 CACCACGGTCAAGAGAGAGACAAATCGCCCTATGACAGGATCGTCTTTAGAGGACAAAA 509
Db 206 CACCACGGTCAAGAGAGAGACAAATCGCCCTATGACAGGATCGTCTTTAGAGGACAAAA 147
QY 510 TATTGTCAACTCTGGTGTCTCAATCAAACTCGTCTTTGATTTCCAGAAAGCTTTACAG 569
Db 146 TATTGTCAACTCTGGTGTCTCAATCAAACTCGTCTTTGATTTCCAGAAAGCTTTACAG 87
QY 570 GTTGTCTGAATCGAAGGCCCTGG 592
Db 86 GTTGTCTGAATCGAAGGCCCTGG 64

RESULT 6
BE048177 666 bp mRNA linear EST 20-OCT-2000
LOCUS BE048177
DEFINITION t246h09.y1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2291681 5',
similar to SW:DH22_HUMAN Q13609 DNASE I HOMOLOGOUS PROTEIN DHP2
PRECURSOR ;, mRNA sequence.
ACCESSION BE048177
VERSION BE048177.1 GI:8365155
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 666)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Insert Length: 1048 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 431.
Location/Qualifiers
1..666
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2291681"
/clone_lib="NCI_CGAP_Brn52"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; This library represents the normalized
version of NCI CGAP Brn35. Cloned unidirectionally.
Primer: oligo dt. Average insert size 1.19 kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(grade II), medulloblastoma, astrocytoma (grade IV)."
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BASE COUNT 198 a 149 c 170 g 147 t 2 others
ORIGIN

Query Match 73.0%; Score 432; DB 10; Length 666;
Best Local Similarity 87.5%; Pred. No. 3,4e-115;
Matches 471; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 1 GAGAGCTAAACGAAATTCAGAAAGGACATATCATATCAATATGATTTAGCTTCGC 60
DB 121 GAGAGCTAAACGAAATTCAGAAAGGACATATCATATGATTTAGCTTCGC 180
QY 61 CTGGAAGAAACACATATTAAGAAACAGTATGCTTTCTATTAAGAAAGAACTAGTCT 120
DB 181 CTGGAAGAAACACATATTAAGAAACAGTATGCTTTCTATTAAGAAAGAACTAGTCT 240
QY 121 GTAAACAAAGCTATCTTACACAGATATATGAGCTGAGAGCGAGATGTGTTTCCAGG 180
DB 241 GTAAAGAGAGTTATCTACATGACTATCAGATGAGAGCGAGATGTGTTTCCAGG 300
QY 181 GAACCTTTTGTGCTGTGCTTCCAGTACACCTTACACCGCTGTCAAGAGCTTGTGATTTGC 240
DB 301 GAGCCCTTTGTGCTGTGCTTCCAGTACACCTTACACCGCTGTCAAGAGCTTGTGATTTGC 360
QY 241 CCCCTGACACACCCCTGAGACATCCGTTAAGAGATTGATGAGTGTGATGCTTAC 300
DB 361 CCCCTGACACACCCCTGAGACATCCGTTAAGAGATTGATGAGTGTGATGCTTAC 420
QY 301 ACAGATGTGAAGCTGCTGCTGATGATGAGAGAAATTTTCAATGAGTGTGATGCTTAC 360
DB 421 ACAGATGTGAAGCTGCTGCTGATGATGAGAGAAATTTTCAATGAGTGTGATGCTTAC 480
QY 361 GGCTGACACTACGCTCCCAAGAAAGGCTTGAAGAGACATCCGCTGAGAGAGAGAGAGAG 420
DB 481 GGCTGACACTACGCTCCCAAGAAAGGCTTGAAGAGACATCCGCTGAGAGAGAGAGAGAG 540
QY 421 TTGCTTTGCTGATGAGGAGCAAGAGAGACACACCGTTCAGAGAGAGAGAGAGAGAG 480
DB 541 TTGCTTTGCTGATGAGGAGCAAGAGAGACACACCGTTCAGAGAGAGAGAGAGAGAG 600
QY 481 TATGACAGGATGTGCTTGAAGAGCAAGAAATGCGAGTTCTGTGTTCCCAAGTCAA 538
DB 601 TATGACAGGATGTGCTTGAAGAGCAAGAAATGCGAGTTCTGTGTTCCCAAGTCAA 658

RESULT 7
BI522352/c 695 bp mRNA linear EST 29-AUG-2001
LOCUS 603081420T1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220532 3',
DEFINITION mRNA sequence.
ACCESSION BI522352
VERSION BI522352.1 GI:15347144
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 695)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LAM11554 row: h column: 05
High quality sequence start: 18
High quality sequence stop: 695.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source Location/Qualifiers
1. 695
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5220532"
/clone_11b="NIH_MGC_120"
/lab_host="DH10B"

/note="Organ: pooled pancreas and spleen; Vector:
pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen) Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 159 a 171 c 163 g 202 t
ORIGIN

Query Match 71.1%; Score 421; DB 13; Length 695;
Best Local Similarity 87.2%; Pred. No. 5.7e-112;
Matches 436; Conservative 0; Mismatches 70; Indels 3; Gaps 3;

QY 23 GAAAGGATTAACATACATATATGATTAAGCTCTGCGCTTGAGAGAAACATATTAAG 82
DB 695 GAGAGGATTAACATACATATATGATTAAGCTCTGCGCTTGAGAGAAACATATTAAG 636
QY 83 AACATATGCTTTCTCTATTAAGAAAGAGTATGCTGTAACAAAGTACTTAC 142
DB 635 CACAAATATGCTTTCTCTATTAAGAAAGAGTATGCTGTAACAAAGTACTTAC 576
QY 143 ACAGATACAGGCTGAGAGAGAGAGATGTGTTTCCAGGAGAACCTTGTGCTGCTTC 202
DB 575 ATGACTATACAGATGAGAGAGAGAGATGTGTTTCCAGGAGAACCTTGTGCTGCTTC 516
QY 203 AGTACCTCTACA-CGCTGTCAAGACCTTGTGATTTGCTCCCTGACACACCCCTGAG 261
DB 515 AATCTCCCAATCTCTGTCGTAAGAAAGCTTGTGATTTATCCCTGACACACCCAGAG 456
QY 262 ACATCCGTTAAGAGATGATGATGCTGCT-GATGCTACACAGATGTAAAGTGTGCTG 320
DB 455 ACATCCGTTAAGAGATGATGATGCTGCTGATGAGGCTTACAGAGAGTAAACACCGCTG 396
QY 321 GAATGACAGAAATTTCAATTTTCAATGAGTGTGCTTCAATGAGTGTGAGTGTGCTTCA 380
DB 395 GAGGCGGAGAAATTTCAATTTTCAATGAGTGTGCTTCAATGAGTGTGAGTGTGCTTCA 336
QY 381 GAGGCGTGAAGAGATCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 440
DB 335 GAGGCGTGAAGAGATCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276
QY 441 CCAAGAGAGACACCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
DB 275 CCAAGAGAGACACCGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 216
QY 501 AGGACAAATATTTGTAACCTGCTGCTGCTCAATCA-AACCTCGCTTGAATTTCCAGA 559
DB 215 AGGACAAATATTTGTAACCTGCTGCTGCTCAATCA-AACCTCGCTTGAATTTCCAGA 156
QY 560 AACCTTACAGGTTTCTGAATGAAGGCC 588
DB 155 AACCTTACAGGTTTCTGAATGAAGGCC 127

RESULT 8
AW543356/c 642 bp mRNA linear EST 31-AUG-2000
LOCUS C0168H07-3 NIH Mouse E7.5 Extraembryonic Portion cDNA Library Mus
DEFINITION muscular cDNA clone C0168H07 3', mRNA sequence.
ACCESSION AW543356
VERSION AW543356.1 GI:7185773
KEYWORDS EST.
SOURCE house mouse.

ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 642)	
REFERENCE AUTHORS	Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H., Ili, Becker, K.G. and Ko, M.S.H.	
	Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse development cDNA microarray	
JOURNAL MEDLINE COMMENT	Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)	
	20381348	
FEATURES	Contact: George J. Kargul	
	Laboratory of Genetics	
source	National Institute on Aging/National Institutes of Health	
	333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA	
Location/Qualifiers	Email: cdna@lgun.grc.nia.nih.gov	
	Plate: Col68 row: H column: 07	
1. 642	Seq primer: -21M13 Forward	
	High quality sequence stop: 642	
POLYA=Yes.	Location/Qualifiers	
	1. 642	
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	/db_xref="nlabST:C0168H07-3"	
/db_xref="taxon:10090"	/clones="C0168H07"	
	/clone.lib="NIA Mouse E7.5 Extraembryonic Portion cDNA Library"	
/sex="unknown"	/dev.stage="7.5dpc Embryo"	
	/lab_host="DH10B"	
/note="Vector: pSPORT1 (Gibco/BRL Life Technology); Site 1: SalI; Site 2: NotI; Total RNAs were extracted from 5 EPC. The double-stranded cDNA was synthesized by Gibco's kit with an Oligo(dT) primer [NotI primer-adaptor from GibcoBRL]	[5'-pGACTAGTCTAGATCGCGAGCGCCCTTTT-3']	
	from 0.8ug of mRNA. The double-stranded cDNAs were treated with T4 DNA polymerase and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Li-Sal3 (include SalI sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Taq polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centricon 100. The cDNAs were digested with SalI and NotI enzymes. Then, the cDNAs were size selected by Gibco's Size Fractionation Column. The cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang."	
BASE COUNT	166 a	161 c 148 g 167 t
	ORIGIN	
Query Match	69.5%;	Score 411.6; DB 10; Length 642;
	Best Local Similarity	83.3%; Pred. No. 3.1e-109;
Matches 468; Conservative	0;	Mismatches 94; Indels 0; Gaps 0;
	QY 31 ATAACTACAACTATGTGATTAGCTCTCGCTTGGAGAAACACATATATAAGACAGTAT 90	
Db	642	ACAACATACAACTATGTGATTAGCTCTCGCTTGGAGAAACACATATATAAGACAGTAT 583
	QY 91 GCCTTTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACCTCTTACACGACTAT 150	
Db	582	GCCTTCGCTCTACAAGAGAAGCTGGTGTCTGTGAACACAAATACCACCTACCATGACTAT 523
	QY 151 CAGGCTGGAGACCGCATGTGTTTCCAGGAACCCCTTTGTGGTCTGGTTCAGTCACCC 210	
Db	522	CAGGATGGAGACACACAGCTGTTTCCAGGGAGCCCTTTGTGGTGTGGTTCATTCCTCC 463
	QY 211 TACACCCTGTCAAGACTTCGTGATTGTGTCCTCCCTGCACACACCCCTGAGACATCCGTT 270	

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Qy 1 GAGAGCTAAACGAAATTCAGAAAAGCATACATACATATGATAGCTCTGC 60
Db 221 GAGAGCTGATGAAATTCACGAAAGACAAATATACATATGATAGCTCTCGA 280
Qy 61 CTTGGAGAAACACATATTAAGAAAGATAGCTCTCTCTATTAAGAAAGATAGTCT 120
Db 281 CTTGGAGAAACACATATTAAGAAAGATAGCTCTCTCTCTATTAAGAAAGATAGTCT 340
Qy 121 GTAAACAAAGCTACCTCTACACAGCATATCAGCTGAGAGCGAGATGTTTCCAG 180
Db 341 GTGAGACAAATATACATACATGATAGATGAGACACAGACGTGTTTCCAG 400
Qy 181 GAAACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 401 GAGCCCTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTG 460
Qy 241 CCCTGACACACACCTGAGACATCCGTTAGAGATGATGAGCTGCTGATGTTAC 300
Db 461 CCCTGACACACACCTGAGACATCCGTTAGAGATGATGAGCTGCTGATGTTAC 520
Qy 301 ACAGATGTAAGCGTGGCTGTAATGAGAAATTCATTTTCAAGGTTCAATGCT 360
Db 521 ACAGATGTAAGCGTGGCTGTAATGAGAAATTCATTTTCAAGGTTCAATGCT 580
Qy 361 GGCTGACGTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
Db 581 GGCTGACGTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640
Qy 420 GTTCG-TTTGGCTGATGGGACCAAGAGACACACGCTGACAGAGACAACTGGC 478
Db 641 GTTCGTTTGGCTGATGGGACCAAGAGACACACGCTGACAGAGACAACTGGC 700
Qy 479 CCTATGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
Db 701 CCTATGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
Qy 539 ACCTGCTTTGATTTTCCAGAAAGCTTACAGTTGCTGATCGAAGGCC 588
Db 761 GTGGCGCTTTGATTTTCCAGAAAGCTTACAGTTGCTGATCGAAGGCC 810

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RESULT 10
BG530136 825 bp mRNA linear EST 03-APR-2001
LOCUS 602558626f1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:469638 5',
DEFINITION mRNA sequence.
ACCESSION BG530136
VERSION BG530136
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 825)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: L1CM1524 row: c column: 07
High quality sequence stop: 743.
Location/Qualifiers
1.825

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FEATURES

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source
/db_xref="taxon:9606"

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/clone="IMAGE:469638"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: testis; Vector: pNR-LIB (Clontech); Site:1:
Site1 (ggccgctggcc); Site2: Site1 (ggccatagggc);
Double-stranded cDNA was prepared from cell line RN. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGAGCGCCGCGACATG-3' (30) BN-3'
(where B = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

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BASE COUNT 225 a 204 c 217 g 179 t
ORIGIN
Query Match 67.0%; Score 396.4; DB 12; Length 825;
Best Local Similarity 82.5%; Pred. No. 9.5e-105;
Matches 490; Conservative 0; Mismatches 101; Indels 3; Gaps 3;

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Qy 1 GAGAGCTAAACGAAATTCAGAAAAGCATACATACATATGATAGCTCTGC 60
Db 232 GAGAGCTGAAACGAAATTCAGAAAAGCATACATACATATGATAGCTCTGC 291
Qy 61 CTTGGAGAAACACATATTAAGAAAGATAGCTCTCTCTATTAAGAAAGATAGTCT 120
Db 292 CTTGGAGAAACACATATTAAGAAAGATAGCTCTCTCTCTATTAAGAAAGATAGTCT 351
Qy 121 GTAAACAAAGCTACCTCTACACAGCATATCAGGCTGG-AGACGAGATGTTTCCAG 179
Db 352 GTAAACAAAGCTACCTCTACACAGCATATCAGGCTGG-AGACGAGATGTTTCCAG 411
Qy 180 GGAACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 239
Db 412 GGAACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
Qy 240 CCCCTGACACACACCTGAGACATCCGTTAGAGATGATGAGCTGCTGATGCTA 299
Db 472 CCCCTGACACACACCTGAGACATCCGTTAGAGATGATGAGCTGCTGATGCTA 531
Qy 300 CACAGATGTAAGCGTGGCTGGAATGACAGAAATTCATTTTCAAGGTTCAATGC 359
Db 532 CACAGATGTAAGCGTGGCTGGAATGACAGAAATTCATTTTCAAGGTTCAATGC 591
Qy 360 TGCTGACGTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
Db 592 TGCTGACGTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
Qy 419 AGTTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
Db 652 AGTTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 711
Qy 479 CCTATGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
Db 712 CCTATGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
Qy 538 AACCTGCTTTGATTTTCCAGAAAGCTTACAGTTGCTGATTCGAAGCCCTTG 591
Db 772 AACCTGCTTTGATTTTCCAGAAAGCTTACAGTTGCTGATTCGAAGCCCTTG 825

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RESULT 11
AM543802 620 bp mRNA linear EST 31-AUG-2000
LOCUS C0174C07-3 NIH Mouse E7.5 Extraembryonic Portion cDNA Library Mus
DEFINITION muscularis cDNA clone C0174C07 3', mRNA sequence.
ACCESSION AM543802
VERSION AM543802.1 GI:7186219
KEYWORDS EST.
SOURCE house mouse.

```

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 620)
AUTHORS Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac
M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Dol,H., Wood,W.H.
III, Becker,K.G. and Ko,M.S.H.
TITLE Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
MEDLINE 20381348
COMMENT Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0174 row: C column: 07
Seq primer: -21M13 Forward
High quality sequence stop: 620
POLYA=Yes.
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
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/clone="C0174C07"
/clone_lib="NIA Mouse E7.5 Extraembryonic Portion cDNA
Library"
/sex="unknown"
/dev_stage="7.5dpc Embryo"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Gibco/BRL Life Technology);
Site 1: SalI; Site 2: NotI; Total RNAs were extracted from
5 EFC. The double-stranded cDNA was synthesized by
Gibco's kit with an Oligo(dT) primer [NotI primer-adaptor
from Gibco/BRL]
[5'-pGACTAGTCTAGATCGGCGGCCCTTTTCTTTT-3']
from 0.8ug of mRNA. The double-stranded cDNAs were
treated with T4 DNA polymerase and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker Ld-Sal3 (include SalI sequence). The cDNAs
were purified by phenol/chloroform and separated from
free linkers by Centricon 100. Then, cDNAs were amplified
by long-range high fidelity PCR using Takara's Ex Taq
polymerase. Then, the cDNAs were purified by
phenol/chloroform and by Centricon 100. The cDNAs were
digested with SalI and NotI enzymes. Then, the cDNAs were
size selected by Gibco's Size Fractionation Column. The
cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by chemical method. The library was
constructed by Xiaohong Wang."

BASE COUNT 160 a 159 c 143 g 158 t
ORIGIN
Query Match 66.1%; Score 391.2; DB 10; Length 620;
Best Local Similarity 82.8%; Pred. No. 2.8e-103;
Matches 447; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 53 GCTCTGCTGGAAGAAACACATATAAAGACAGATGCTCTTCTCTATAAAGAAAGC 112
DB 620 GTTCTCGATGTGAAGAAACACATATAAAGACAGATGCTCTTCTCTATAAAGAAAGC 561
QY 113 TAGTGTCTGTAAACAAAGTACTCTTACCACGACTATCAGGCTGGAGCGGAGATGTTT 172
DB 560 TGTGTCTGTGAGACAAATACCACTACCTATCAGGATGAGACACAGAGCTGT 501
QY 173 TTTCCAGGGAACCTTTGTGGTCTGGTCCAGTCCACCTACCGCTGTCAAGGACTTCG 232
DB 500 TTTCCAGGGAACCTTTGTGGTCTGGTCCAGTCCACCTACCGCTGTCAAGGACTTCG 441
QY 233 TGATTGTCCTCGACACCAACCCCTGAGACATCCGTTAGAGAGATTGATGCTGGCTG 292

Db 440 TGATTGTCCTCGACACAACTCCGAGACTCCGTTAAAGAGATAGATGCTGGTCG 381
QY 293 ATGTCTACACAGATGTGAACAGTCCGCTGGAATGAGAGAAATTTCAATTTTATGGTGACT 352
Db 380 ATGTCTACACAGGATGTGAGAGCCAGTGTGAAGACAGAGAAATTTCAATTTTATGGTGACT 321
QY 353 TCAATGCTGGCTGAGCTACGTCCTCCCAAGAGGCTTGAAGGACATCCGCTGAGGACGG 412
Db 320 TCAAGCGCGCTGTAGCTATGTCCTCCCAAGAGGCTTGAAGGACATCCGTTGAGGACGG 261
QY 413 ACCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACCAACCGTCAAGAGACACAA 472
Db 260 ACCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGACCAACCGTCAAGAGATACCA 201
QY 473 ACTGCGCTTATCAGAGATCGTGTAGAGGACAAAATTTGTCAACTCTGTTGCTC 532
Db 200 GCTGTGCTTATGACAGGATGTGCTTTGTGGACAAGAGATAGTCACTCCGTTGACCCC 141
QY 533 AATCAACCTCGCTTGTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 592
Db 140 GTTCCAGTGGCGTCTTTGACTTTTCAGAAAGCTTATGACTTTGCTGAGGAGGAGCCCTGG 81
RESULT 12
BI460950 603207187F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272917 5',
LOCUS mRNA sequence.
DEFINITION BI460950
ACCESSION BI460950
VERSION BI460950.1 GI:15251606
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 628)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11688 row: n column: 22
High quality sequence stop: 628.
FEATURES
source Location/Qualifiers
1..628
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/db_xref="taxon:9606"
/clone="IMAGE:5272917"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 181 a 144 c 166 g 137 t
ORIGIN
Query Match 65.8%; Score 389.4; DB 13; Length 628;
Best Local Similarity 90.1%; Pred. No. 9.4e-103;

	Matches	417;	Conservative	0;	Mismatches	46;	Indels	0;	Gaps	0;
Qy	1	GAGAGCTTAAACGGAAATTCAGAAAAAGGCATTAACATAACTATGTGATTAGCTTCGCC	60							
Db	166	GAGAGGCTGTAAGAGAAATTCAGAGAGAGGCATTAACATAACTATGTGATTAGCTTCGG	225							
Qy	61	CTTGGAGAAACACATATTAAGAACAGTATGCTTCTCTATATAAGAAAGCTAGTGTCT	120							
Db	226	CTTGGAGAGAAACACATATTAAGAACATATATGCTTCTCTACAGSAAAAGCTGAGTCT	285							
Qy	121	GTAATAACAAGTACTACTTACCAACCATATCAAGCTGTGAGAGCGCAGATGTGTTTCCAG	180							
Db	286	GTAAGAGAGGATTATCATCAATCATATGACTATACAGAGAGAGACGCAATATGTGTTTCCAG	345							
Qy	181	GAACCTTTTGTTGTTGTTGTTCCAGTACACCCCTACACCGCTCAAGGACTCGTGATTGTC	240							
Db	346	GAGCCCTTTTGTTGTTGTTGTTCCATCTCTCCCACTCTGCTCTAAAGACTCTTGATTATTC	405							
Qy	241	CCCCCTGCACACCAACCCCTGCAGACATCCGTTAGAGAGATTGATGAGCTGATGTTCTAC	300							
Db	406	CCCCGCACACCAACCCCAAGAGACATCCGTTAAGAGAGATTGATGAGTGGTTGAGGCTTAC	465							
Qy	301	ACAGATGTGAAACGTGCTGCTGGAATGAGAGATTTTCATTTTATGSGGTACTTCATGTGT	360							
Db	466	ACGAGACGTGAAACACCGCTGGAAGCGGAGAAATTTTCATTTTATGSGGTACTTCATGTGCC	525							
Qy	361	GGCTGCAGCTACGTCCCCCAAGAAAGCTTGAAGACATCCGCTTGAGAGCGAGACCCCAAG	420							
Db	526	GGCTGCACACTACGTCCCCCAAGAAAGCCTTGAAGAAACATCCGCTTGAGAGACTGACCCCAAG	585							
Qy	421	TTTCGTTTGCTGATCGGGGACCCAGAGGACACACGGGTCAAGA	463							
Db	586	TTTGTGTTGCTGATCGGGGACCCAGAGGACACACGGGTCAAGA	628							

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ACCESSION      AW915564
VERSION        AW915564.1  GI:8081263
KEYWORDS
SOURCE
ORGANISM       Rattus sp.
               Rattus sp.
REFERENCE      1 (bases 1 to 668)
AUTHORS        Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
               Kerlavage,A.R. and Adams,M.D.
TITLE          Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
               Gene Index
JOURNAL        Unpublished (1998)
COMMENT        Contact: Lee, NH
               The Institute for Genomic Research
               9712, Medical Center Drive, Rockville, MD 20850, USA
               Tel: (301)-838-3529
               Fax: (301)-838-0208
               Email: nhlee@tigr.org
               This clone is available through the ATCC, contact the ATCC
               tel#703-365-2700 for further information
               Seq primer: M13 Reverse.
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PRECURSOR ;, mRNA Sequence.
ACCESSION      AI927844
VERSION        AI927844.1  GI:5663808
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SOURCE         human.
ORGANISM       Homo sapiens
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REFERENCE      1 (bases 1 to 784)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgabbs-r@mail.nih.gov
               Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
               Emmert-Buck, M.D., Ph.D.
               cDNA Library Preparation: M. Bento Soares, Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
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               hybridization reaction. The driver was PCR-amplified cDNAs
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               (cloneids 1322376-1323911, 1456007-1456775, and
               1500552-1502855). Subtraction by Bento Soares and M.
               Fatima Bonaldo."
BASE COUNT    173 a 188 c 179 g 242 t 2 others
ORIGIN
Query Match   64.8%; Score 383.6; DB 9; Length 784;
Best Local Similarity 86.7%; Pred. No. 5.1e-101;
Matches 422; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

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Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	149.4	25.2	1039	4	US-09-638-112-2 Sequence 2, Appl
5	149.4	25.2	1039	5	PCT-US93-05136-2 Sequence 2, Appl
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7	147.8	25.0	1039	1	US-08-458-367-2 Sequence 2, Appl
8	117.2	19.8	1615	2	US-08-491-988-15 Sequence 1, Appl
9	117.2	19.8	1624	2	US-08-491-988-14 Sequence 1, Appl
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ALIGNMENTS

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US-08-640-765A-2
Sequence 2, Application US/08640765A
Patent No. 5821103
GENERAL INFORMATION:
APPLICANT: Tanuma, Sei-ichi
TITLE OF INVENTION: NOVEL DEOXYRIBONUCLEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Leydig, Volt & Mayer
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,765A
FILING DATE: 06-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6239518
FILING DATE: 06-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Robert F.
REGISTRATION NUMBER: 27555
REFERENCE/DOCKET NUMBER: 73362
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 12..941
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Matches 505; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 85519
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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NAME/KEY: CDS
LOCATION: 12..941
US-09-073-613-2

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Patent No. 6143875
GENERAL INFORMATION:
APPLICANT: Tanuma, Sei-ichi
TITLE OF INVENTION: ANTIBODY TO NOVEL DEOXYRIBONUCLEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Leydig, Voit & Mayer
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,613
FILING DATE: 06-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,765
FILING DATE:
APPLICATION NUMBER: JP 6239518
FILING DATE: 06-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: LARCHER, Carol

Qy	34	ACATACAACTATGTGATTAGCTCTCGCCTTGGAGAAACACATATAAAGACAGTATGCC	93
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Db 1555 CTTTGAACGAATGGCGCTGG 1576

RESULT 10

US-08-491-988-13
; Sequence 13, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMENNON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,988
; FILING DATE: 18-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDBERG, JULES E.
; REGISTRATION NUMBER: 24,408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-986-4090
; TELEFAX: 212-818-9479
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1648 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-08-491-988-13

Query Match 19.8%; Score 117.2; DB 2; Length 1648;
Best Local Similarity 53.0%; Pred. No. 6,6e-27;
Matches 298; Conservative 0; Mismatches 258; Indels 6; Gaps 2;

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Qy 271 AGAGAGATTGATGAGCTGCTGATGCTTACACAGATGTGAAGCGTCTGAAATGACAG 330
Db 1282 GCTGAATCACTCTCTGTACGACGTTTACCTGACGTTCCAGCAAGAAATGGCAGCTGAAC 1341
Qy 331 AATTGATTTTCAATGGGTGCTTCAATGCTGCTGAGCTAGCTGCCCAAGAAAGCCCTGG 390
Db 1342 GACGTATGCTGTGAGGCTGACTTCAACGCTGACTGCTTATGTAACTCTTCTCAATGG 1401
Qy 391 AAGGAGATCCGCTGAGAGACCCCAAGTTCGTTGGCTGATCGGGGACCAAGAGAC 450
Db 1402 TCATGATTGCTGTGGACCTGCTGACCTTCCAGTGGCTATCCGAGCTCCGCTGAC 1461
Qy 451 ACCAGGTCAGAGAGACCAACTGCGCTTATGACAGATGTGCTTACAGACAAAT 510
Db 1462 ACCACCGCTACT--AGTACCAACTGGGCTTACGACCGTATGCTGTGCTGATCCCTG 1518
Qy 511 ATTGCACTCTGGGTGCTCTCAATCAAACTCGCTTTGATTTCCAGAAAGCTTACAG 570
Db 1519 CTCGAGCTCTTCTGTGTACCGGAGCGGCGCCGTTGCACTTCCAGGCTGATATGCT 1578
Qy 571 TTGCTGATCGAAGGCCCTGG 592
Db 1579 CTTTGAACGAATGGCGCTGG 1600

RESULT 11

US-08-468-012A-1
; Sequence 1, Application US/08468012A
; Patent No. 5830744
; GENERAL INFORMATION:
; APPLICANT: RUBEN, ET AL.
; TITLE OF INVENTION: Human DNase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,012A
; FILING DATE: 6 JUNE 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04954

Mon Dec 9 13:45:01 2002

;; FILING DATE: 5 MAY 1994
;; APPLICATION NUMBER: PCT/US94/04954
;; FILING DATE: 5 MAY 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MULLINS, J.G.
;; REGISTRATION NUMBER: 33,073
;; REFERENCE/DOCKET NUMBER: 325800-428
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1055 BASE PAIRS
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: SINGLE
;; TOPOLOGY: LINEAR
;; MOLECULE TYPE: CDNA
US-08-468-012A-1

Query Match 19.5%; Score 115.2; DB 2; Length 1055;
Best Local Similarity 58.6%; Pred. No. 2.2e-26;
Matches 198; Conservative 1; Mismatches 139; Indels 0; Gaps 0;
QY 160 GAGCAGATGCTTTTCCAGGAACCTTTGGTCTGCTCCAGTCACCCCTACACCGCT 219
Db 359 GAGGATGACGCTTTTGGCCGGAGCCATTGTTGGCCCACTTCTTTGCCAGCAATGTC 418
QY 220 GTCAAGGACTTCGTGATGTTCCACACACACACCCCTGACATCCGTTAGAGATT 279
Db 419 CTTCCAGCTGCTGTTGCTCCGCTGACACACCTCTCTAAGCCGTAGAGAAGAGCTG 478
QY 280 GATGAGCTGGCTGATCTACACAGATGTGAAACGCTGGAATGCAGAGAAATTTTATT 339
Db 479 AAGCCCTCTACGATGTTCTGAGAGTCTCCAGCACTGGCAGCAAGAGAGCTG 538
QY 340 TTTCATGGTGAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
Db 539 CTGCTGGGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
QY 400 CGCTGAGGAGCAACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459
Db 599 GSGCTGCGGACTGAGCAGGCTTCCACTGGTGAITGGCGATGGGAGGACACCAAGTG 658
QY 460 AAGAAGACACAACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 497
Db 659 CGGCCAGCACCACTGACCTATGACCGCTGCTGCT 696

RESULT 12
US-09-054-989-1
Sequence 1, Application US/09054989
Patent No. 6251648
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Human Dnase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OUSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,989
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,012

;; FILING DATE: 6-JUNE-1995
;; APPLICATION NUMBER: PCT/US94/04954
;; FILING DATE: 5 MAY 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MULLINS, J.G.
;; REGISTRATION NUMBER: 33,073
;; REFERENCE/DOCKET NUMBER: 325800-428
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1055 BASE PAIRS
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: SINGLE
;; TOPOLOGY: LINEAR
;; MOLECULE TYPE: CDNA
US-09-054-989-1

Query Match 19.5%; Score 115.2; DB 4; Length 1055;
Best Local Similarity 58.6%; Pred. No. 2.2e-26;
Matches 198; Conservative 1; Mismatches 139; Indels 0; Gaps 0;
QY 160 GAGCAGATGCTTTTCCAGGAACCTTTGGTCTGCTCCAGTCACCCCTACACCGCT 219
Db 359 GAGGATGACGCTTTTGGCCGGAGCCATTGTTGGCCCACTTCTTTGCCAGCAATGTC 418
QY 220 GTCAAGGACTTCGTGATGTTCCACACACACACCCCTGACATCCGTTAGAGATT 279
Db 419 CTTCCAGCTGCTGTTGCTCCGCTGACACACCTCTCTAAGCCGTAGAGAAGAGCTG 478
QY 280 GATGAGCTGGCTGATCTACACAGATGTGAAACGCTGGAATGCAGAGAAATTTTATT 339
Db 479 AAGCCCTCTACGATGTTCTGAGAGTCTCCAGCACTGGCAGCAAGAGAGCTG 538
QY 340 TTTCATGGTGAATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
Db 539 CTGCTGGGAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
QY 400 CGCTGAGGAGCAACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459
Db 599 GSGCTGCGGACTGAGCAGGCTTCCACTGGTGAITGGCGATGGGAGGACACCAAGTG 658
QY 460 AAGAAGACACAACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 497
Db 659 CGGCCAGCACCACTGACCTATGACCGCTGCTGCT 696

RESULT 13
US-09-173-581-10
Sequence 10, Application US/09173581A
Patent No. 6013455
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina
APPLICANT: Azimzal, Yalda
APPLICANT: Lu, Aina
TITLE OF INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
CURRENT APPLICATION NUMBER: US/09/173,581A
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 1427
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -

OTHER INFORMATION: 119819
US-09-173-581-10

Query Match
Best Local Similarity 53.7%; Score 35.2; DB 3; Length 1427;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 322 AATGACAGAAATTTTCATTTTCATGGTGAAGTCAATGCTGCTGACGCTACGTCACG 381
DB 857 AATGACAGATTAAGATCAAGATCAAGATGCGACAGCTGGCAACGCTGCTGCTGCAAG 916
QY 382 AAGGCTTGGAAGACATCCGCTGAGAGCGAGCCCAAGTTCTTTGGCTGATCGGAG 441
DB 917 CACTTACGGAACATCCAGACTCGGAGTACCGGCGCTCGAGTGTGATCGGCGCC 976
QY 442 CAAGAGGACACACCG 457
DB 977 GAATACGCGCCCCCG 992

RESULT 14

US-09-420-915-10
Sequence 10, Application US/09420915
Patent No. 6264947
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Guebler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina
APPLICANT: Azimzai, Yalda
APPLICANT: Lu, Aina
TITLE OF INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
CURRENT APPLICATION NUMBER: US/09/420,915
EARLIER FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/173,581
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 1427
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 119819
US-09-420-915-10

Query Match
Best Local Similarity 53.7%; Score 35.2; DB 4; Length 1427;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 322 AATGACAGAAATTTTCATTTTCATGGTGAAGTCAATGCTGCTGACGCTACGTCACG 381
DB 857 AATGACAGATTAAGATCAAGATCAAGATGCGACAGCTGGCAACGCTGCTGCTGCAAG 916
QY 382 AAGGCTTGGAAGACATCCGCTGAGAGCGAGCCCAAGTTCTTTGGCTGATCGGAG 441
DB 917 CACTTACGGAACATCCAGACTCGGAGTACCGGCGCTCGAGTGTGATCGGCGCC 976
QY 442 CAAGAGGACACACCG 457
DB 977 GAATACGCGCCCCCG 992

RESULT 15

US-08-924-440-1
Sequence 1, Application US/08924440
Patent No. 5871550
GENERAL INFORMATION:
APPLICANT: Fitts et al.

TITLE OF INVENTION: MUTANT THERMONOSFORA SPP. CELLULASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,440
FILING DATE: August 27, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Stone
REGISTRATION NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-7555
TELEFAX: (650) 845-6504
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-924-440-1

Query Match
Best Local Similarity 58.0%; Score 32.8; DB 2; Length 1293;
Matches 58; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 351 CTTCATGCTGCTGAGTACGTCCTCCCAAGAGCGCTGGAAGACATCCGCTGAGAC 410
DB 1080 CTACACCGGTGAGCGGCCCAACGACTTCCAGATGCGCGACCGCTACATGACTGATG 1139
QY 411 GGACCCCAAGTTGTTGGCTGATCGGAGGACCAAGAGAC 450
DB 1140 GGACCGAAGATCGGTGAGCAAGTGAATTAATCTGAGAC 1179

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Job time : 52.0918 secs

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2002, 09:00:58 ; Search time 117.65 Seconds
(without alignments)
1962.092 Million cell updates/sec

Title: US-09-905-114-1

Perfect score: 592
Sequence: 1 gagaagcctaacggaattc.....gtctgacgaagccctcg 592

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Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 19496369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	592	100.0	592	10	US-09-905-114-1
2	592	100.0	671	10	US-09-905-114-3
3	476.8	80.5	1023	10	US-09-962-436-336
4	476.8	80.5	1023	10	US-09-954-456-271
5	476.8	80.5	1023	10	US-09-880-107-3392
6	476.8	80.5	1079	12	US-10-133-065-1
7	476.8	80.5	1079	12	US-10-074-509-1
8	435.2	73.5	1124	12	US-10-133-065-11
9	435.2	73.5	1124	12	US-10-074-509-11
c 10	171.4	25.0	392	10	US-09-880-107-610
11	149.4	25.2	1039	10	US-09-771-078-1
12	149.4	25.2	1039	10	US-09-825-012-2
13	147.8	25.0	783	10	US-09-825-012-4
14	147.8	25.0	858	10	US-09-825-012-6
15	147.8	25.0	1548	10	US-09-825-012-62
16	147.8	25.0	1548	10	US-09-825-012-63
17	147.8	25.0	1548	10	US-09-825-012-65
18	147.8	25.0	1554	10	US-09-825-012-34
19	147.8	25.0	1554	10	US-09-825-012-35

20	147.8	25.0	1554	10	US-09-825-012-37	Sequence 37, Appl
21	147.8	25.0	1557	10	US-09-825-012-64	Sequence 64, Appl
22	147.8	25.0	1560	10	US-09-825-012-72	Sequence 72, Appl
23	147.8	25.0	1560	10	US-09-825-012-73	Sequence 73, Appl
24	147.8	25.0	1560	10	US-09-825-012-75	Sequence 75, Appl
25	147.8	25.0	1560	10	US-09-825-012-77	Sequence 77, Appl
26	147.8	25.0	1560	10	US-09-825-012-78	Sequence 78, Appl
27	147.8	25.0	1560	10	US-09-825-012-79	Sequence 79, Appl
28	147.8	25.0	1563	10	US-09-825-012-36	Sequence 36, Appl
29	147.8	25.0	1566	10	US-09-825-012-67	Sequence 67, Appl
30	147.8	25.0	1566	10	US-09-825-012-68	Sequence 68, Appl
31	147.8	25.0	1566	10	US-09-825-012-70	Sequence 70, Appl
32	147.8	25.0	1569	10	US-09-825-012-74	Sequence 74, Appl
33	147.8	25.0	1575	10	US-09-825-012-69	Sequence 69, Appl
34	147.8	25.0	1578	10	US-09-825-012-81	Sequence 81, Appl
35	147.8	25.0	1578	10	US-09-825-012-82	Sequence 82, Appl
36	147.8	25.0	1578	10	US-09-825-012-84	Sequence 84, Appl
37	147.8	25.0	1584	10	US-09-825-012-39	Sequence 39, Appl
38	147.8	25.0	1584	10	US-09-825-012-40	Sequence 40, Appl
39	147.8	25.0	1584	10	US-09-825-012-42	Sequence 42, Appl
40	147.8	25.0	1587	10	US-09-825-012-83	Sequence 83, Appl
41	147.8	25.0	1590	10	US-09-825-012-91	Sequence 91, Appl
42	147.8	25.0	1590	10	US-09-825-012-92	Sequence 92, Appl
43	147.8	25.0	1590	10	US-09-825-012-94	Sequence 94, Appl
44	147.8	25.0	1593	10	US-09-825-012-41	Sequence 41, Appl
45	147.8	25.0	1596	10	US-09-825-012-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-09-905-114-1
; Sequence 1, Application US/09905114
; Patent No. US20020046745A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, HUANNIN
; APPLICANT: AX, ROY L
; APPLICANT: BELIN, MARY E
; TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDE SEQUENCES ENCODING A FERTILITY ASSOCIATED
; FILE REFERENCE: 2107070520
; CURRENT APPLICATION NUMBER: US/09/905,114
; CURRENT FILING DATE: 2001-07-14
; PRIOR APPLICATION NUMBER: US 60/218,140
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Bos sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION:
US-09-905-114-1

Query Match 100.0%; Score 592; DB 10; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.2e-176;
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GAGAACTAAAGCGAATTCAGAAAGCATACATACATGATGTTACTCTCGC	60
DB	1	GAGAACTAAAGCGAATTCAGAAAGCATACATACATGATGTTACTCTCGC	60
QY	61	CTTGAAGAAACATATTAAGACAGTATGCTTCTATTAAGAAAGCTAGTGTCT	120
DB	61	CTTGAAGAAACATATTAAGACAGTATGCTTCTATTAAGAAAGCTAGTGTCT	120
QY	121	GTTAAACAAAGCTACTCTTACACGACTATCAGGCTGAGAGCAGACATGTTTCCAGG	180
DB	121	GTTAAACAAAGCTACTCTTACACGACTATCAGGCTGAGAGCAGACATGTTTCCAGG	180

QY 181 GAACCTTTTGGTCTGGTTCCAGTCAACCTACACCGCTGTCAAGGACTTCGTGATTGTC 240
DB 181 GAACCTTTTGGTCTGGTTCCAGTCAACCTACACCGCTGTCAAGGACTTCGTGATTGTC 240
QY 241 CCCCTGCACACCCCTTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGATGCTTAC 300
DB 241 CCCCTGCACACCCCTTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGATGCTTAC 300
QY 301 ACAGATGGAACCTCGTGTGAATGCAGAGAAATTCATTTTCATGGGTGACTTCAATGCT 360
DB 301 ACAGATGGAACCTCGTGTGAATGCAGAGAAATTCATTTTCATGGGTGACTTCAATGCT 360
QY 361 GGCTGCAGCTACGTCCTCCCAAGAGCCCTGGAAGGACATCCGCTTGAGGACGACCCCAAG 420
DB 361 GGCTGCAGCTACGTCCTCCCAAGAGCCCTGGAAGGACATCCGCTTGAGGACGACCCCAAG 420
QY 421 TTGCTTTGGCTGATCGGGACCAAGAGACACACCGGTCAAGAGAGACACAACTGGGCC 480
DB 421 TTGCTTTGGCTGATCGGGACCAAGAGACACACCGGTCAAGAGAGACACAACTGGGCC 480
QY 481 TATCAGAGGATCGTGTGAGGACAAATATTGTCAACTCTGGTGTCTCAATCAAAAC 540
DB 481 TATCAGAGGATCGTGTGAGGACAAATATTGTCAACTCTGGTGTCTCAATCAAAAC 540
QY 541 CTGCTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCCAAAGGCCCTGG 592
DB 541 CTGCTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCCAAAGGCCCTGG 592

RESULT 2

US-09-905-114-3
; Sequence 3, Application US/09905114
; Patent No. US20020048745A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, HUANMIN
; APPLICANT: AX, ROY L
; APPLICANT: BELLIN, MARY E
; TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDE SEQUENCES ENCODING A FERTILITY ASSOCIATED
; FILE REFERENCE: 210707US20
; CURRENT APPLICATION NUMBER: US/09/905,114
; PRIOR FILING DATE: 2001-07-14
; PRIOR APPLICATION NUMBER: US 60/218,140
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Bos sp.
US-09-905-114-3

Query Match 100.0%; Score 592; DB 10; Length 671;
Best Local Similarity 100.0%; Pred. No. 1.3e-176;
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGAGCTAAACGGAATTCAGAAAGGCAATACATACACTATGTGATTAGCTCTCGC 60
DB 27 GAGAGCTAAACGGAATTCAGAAAGGCAATACATACACTATGTGATTAGCTCTCGC 86
QY 61 CTTGGAAGAAACACATATAAGAACAGTATGCCCTTCTCTATAAGAAAGCTAGTGTCT 120
DB 87 CTTGGAAGAAACACATATAAGAACAGTATGCCCTTCTCTATAAGAAAGCTAGTGTCT 146
QY 121 GTAAACAAAGCTACCTCTACACAGCTATCAGGCTGGAGACGAGATGTGTTCCAGG 180
DB 147 GTAAACAAAGCTACCTCTACACAGCTATCAGGCTGGAGACGAGATGTGTTCCAGG 206
QY 181 GAACCTTTTGGTCTGGTTCCAGTCAACCTACACCGCTGTCAAGGACTTCGTGATTGTC 240
DB 207 GAACCTTTTGGTCTGGTTCCAGTCAACCTACACCGCTGTCAAGGACTTCGTGATTGTC 266
QY 241 CCCCTGCACACCCCTTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGATGCTTAC 300

DB 267 CCCCTGCACACCCCTTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGATGCTTAC 326
QY 301 ACAGATGGAACCTCGTGTGAATGCAGAGAAATTCATTTTCATGGGTGACTTCAATGCT 360
DB 327 ACAGATGGAACCTCGTGTGAATGCAGAGAAATTCATTTTCATGGGTGACTTCAATGCT 386
QY 361 GGCTGCAGCTACGTCCTCCCAAGAGCCCTGGAAGGACATCCGCTTGAGGACGACCCCAAG 420
DB 387 GGCTGCAGCTACGTCCTCCCAAGAGCCCTGGAAGGACATCCGCTTGAGGACGACCCCAAG 446
QY 421 TTGCTTTGGCTGATCGGGACCAAGAGACACACCGGTCAAGAGAGACACAACTGGGCC 480
DB 447 TTGCTTTGGCTGATCGGGACCAAGAGACACACCGGTCAAGAGAGACACAACTGGGCC 506
QY 481 TATCAGAGGATCGTGTGAGGACAAATATTGTCAACTCTGGTGTCTCAATCAAAAC 540
DB 507 TATCAGAGGATCGTGTGAGGACAAATATTGTCAACTCTGGTGTCTCAATCAAAAC 566
QY 541 CTGCTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCCAAAGGCCCTGG 592
DB 567 CTGCTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCCAAAGGCCCTGG 618

RESULT 3

US-09-962-436-336
; Sequence 336, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signal
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 336
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-336

Query Match 80.5%; Score 476.8; DB 10; Length 1023;
Best Local Similarity 87.8%; Pred. No. 3.1e-140;
Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 GAGAGCTAAACGGAATTCAGAAAGGCAATACATACACTATGTGATTAGCTCTCGC 60
DB 241 GAGAGCTAAACGGAATTCAGAGAGAGGCAATACCGTACAACTATGTGATTAGCTCTCG 300
QY 61 CTTGGAAGAAACACATATAAGAACAGTATGCCCTTCTCTATAAGAAAGCTAGTGTCT 120
DB 301 CTTGGAAGAAACACATATAAGAACAGTATGCCCTTCTCTATAAGAAAGCTAGTGTCT 360
QY 121 GTAAACAAAGCTACCTCTACACAGCTATCAGGCTGGAGACGAGATGTGTTCCAGG 180
DB 361 GTGAAGAGGAGTTATCACTACCATGACTATCAGGATGGAGCGCAGATGTGTTCCAGG 420
QY 181 GAACCTTTTGGTCTGGTTCCAGTCAACCTACACCGCTGTCAAGGACTTCGTGATTGTC 240
DB 421 GAGCCCTTTTGGTCTGGTTCCAACTCTCCCACTCTGTCAAAGACTTCGTGATTATC 480
QY 241 CCCCTGCACACCCCTTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGATGCTTAC 300
DB 481 CCCCTGCACACCCCTTGAGACATCCGTTAGAGAGATCGATGAGTTGGTTGAGGCTTAC 540
QY 301 ACAGATGGAACCTCGTGTGAATGCAGAGAAATTCATTTTCATGGGTGACTTCAATGCT 360
DB 541 ACAGATGGAACCTCGTGTGAATGCAGAGAAATTCATTTTCATGGGTGACTTCAATGCT 600

Oy 361 GCGTCAGCTACGTCCTCCCAAGAGGCGCTGGAAGACATCCGCTGAGAGCGAGCCCCAAG 420
 Db 601 GCGTCAGCTACGTCCTCCCAAGAGGCGCTGGAAGACATCCGCTGAGAGCGAGCCCCAAG 660
 Oy 421 TTCGTTGGCTGATCGGGAGCCAGAGGACACCGGTCAAGAGAGCACAACTGCGCC 480
 Db 661 TTTGTTGGCTGATCGGGAGCCAGAGGACACCGGTCAAGAGAGCACAACTGCGCA 720
 Oy 481 TATGACAGGATGCTGCTTGAAGAGCAAAATATGTCACCTGCTGCTGCTCAATCAAC 540
 Db 721 TATGACAGGATGCTGCTTGAAGAGCAAAATGTCAGTCTGTTGTTCCCAAGTCAAC 780
 Oy 541 CTCGCTTTGATTTCCAGAAAGCTTACAGGTTGCTGAATCGAAGGCCCTGG 592
 Db 781 AGTGTTTGTGACTCCAGAAAGCTTACAGCTGACTGAAGAGAGGCCCTGG 832

RESULT 4

US-09-954-456-271
 : Sequence 271, Application US/09954456
 : Patent No. US20020115057A1
 : GENERAL INFORMATION:
 : APPLICANT: Young, Paul
 : TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
 : FILE REFERENCE: 689290-76
 : CURRENT APPLICATION NUMBER: US/09/954,456
 : CURRENT FILING DATE: 2001-09-18
 : PRIOR APPLICATION NUMBER: US/60/233,617
 : PRIOR FILING DATE: 2000-09-18
 : PRIOR APPLICATION NUMBER: US/60/234,052
 : PRIOR FILING DATE: 2000-09-20
 : PRIOR APPLICATION NUMBER: US/60/234,923
 : PRIOR FILING DATE: 2000-09-25
 : PRIOR APPLICATION NUMBER: US/60/235,134
 : PRIOR FILING DATE: 2000-09-25
 : PRIOR APPLICATION NUMBER: US/60/235,637
 : PRIOR FILING DATE: 2000-09-26
 : PRIOR APPLICATION NUMBER: US/60/235,638
 : PRIOR FILING DATE: 2000-09-26
 : PRIOR APPLICATION NUMBER: US/60/235,711
 : PRIOR FILING DATE: 2000-09-27
 : PRIOR APPLICATION NUMBER: US/60/235,720
 : PRIOR FILING DATE: 2000-09-27
 : PRIOR APPLICATION NUMBER: US/60/235,840
 : PRIOR FILING DATE: 2000-09-27
 : PRIOR APPLICATION NUMBER: US/60/235,863
 : PRIOR FILING DATE: 2000-09-27
 : NUMBER OF SEQ ID NOS: 2276
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 271
 : LENGTH: 1023
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-954-456-271

Query Match 80.5%; Score 476.8; DB 10; Length 1023;
 Best Local Similarity 87.8%; Pred. No. 3.1e-140;
 Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Oy 1 GAGAGCTAAACGGAATTCAGAAAGGATTAACATACATCATGATGATGATGCTCGC 60
 Db 241 GAGAGCTAAACGGAATTCAGAAAGGATTAACATACATCATGATGATGATGCTCGC 300
 Oy 61 CTGGAAGAAACACATATAAAGACGATATGCTTTCTCTATTAAGAAAGGATGCTCT 120
 Db 301 CTGGAAGAAACACATATAAAGACGATATGCTTTCTCTATTAAGAAAGGATGCTCT 360
 Oy 121 GTAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
 Db 361 GTAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420

Oy 181 GAAACCTTTGTGCTGCTGCTTCCAGTCACCTACACCGCTGTCAAGACCTTGTGATGTC 240
 Db 421 GAAACCTTTGTGCTGCTGCTTCCAGTCACCTACACCGCTGTCAAGACCTTGTGATGTC 480
 Oy 241 CCCCTGACACCAACCCCTTACAGATCCGTTAGAGATGATGATGATGATGATGATGATG 300
 Db 481 CCCCTGACACCAACCCCTTACAGATCCGTTAGAGATGATGATGATGATGATGATGATG 540
 Oy 301 ACAGATGTAAGACGTCGCTGGAATGAGAGAAATTTGATTTTCAATGAGGATGATGATG 360
 Db 541 ACAGATGTAAGACGTCGCTGGAATGAGAGAAATTTGATTTTCAATGAGGATGATGATG 600
 Oy 361 GCGTCAGCTACGTCCTCCCAAGAGGCGCTGGAAGACATCCGCTGAGAGCGAGCCCCAAG 420
 Db 601 GCGTCAGCTACGTCCTCCCAAGAGGCGCTGGAAGACATCCGCTGAGAGCGAGCCCCAAG 660
 Oy 421 TTCGTTGGCTGATCGGGAGCCAGAGGACACCGGTCAAGAGAGCACAACTGCGCC 480
 Db 661 TTTGTTGGCTGATCGGGAGCCAGAGGACACCGGTCAAGAGAGCACAACTGCGCA 720
 Oy 481 TATGACAGGATGCTGCTTGAAGAGCAAAATATGTCACCTGCTGCTGCTCAATCAAC 540
 Db 721 TATGACAGGATGCTGCTTGAAGAGCAAAATGTCAGTCTGTTGTTCCCAAGTCAAC 780
 Oy 541 CTCGCTTTGATTTCCAGAAAGCTTACAGGTTGCTGAATCGAAGGCCCTGG 592
 Db 781 AGTGTTTGTGACTCCAGAAAGCTTACAGCTGACTGAAGAGAGGCCCTGG 832

RESULT 5

US-09-880-107-3392
 : Sequence 3392, Application US/09880107
 : Patent No. US20020142981A1
 : GENERAL INFORMATION:
 : APPLICANT: Horne, Darci T.
 : APPLICANT: Vockley, Joseph G.
 : APPLICANT: Scherf, Uwe
 : APPLICANT: Gene Logic, Inc.
 : TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 : FILE REFERENCE: 44921-5028-NO
 : CURRENT APPLICATION NUMBER: US/09/880,107
 : CURRENT FILING DATE: 2001-06-14
 : PRIOR APPLICATION NUMBER: US 60/211,379
 : PRIOR FILING DATE: 2000-06-14
 : PRIOR APPLICATION NUMBER: US 60/237,054
 : PRIOR FILING DATE: 2000-10-02
 : NUMBER OF SEQ ID NOS: 3950
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 3392
 : LENGTH: 1023
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : OTHER INFORMATION: Genbank Accession No. US20020142981A1 US6814
 : US-09-880-107-3392

Query Match 80.5%; Score 476.8; DB 10; Length 1023;
 Best Local Similarity 87.8%; Pred. No. 3.1e-140;
 Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Oy 1 GAGAGCTAAACGGAATTCAGAAAGGATTAACATACATCATGATGATGATGCTCGC 60
 Db 241 GAGAGCTAAACGGAATTCAGAAAGGATTAACATACATCATGATGATGATGCTCGC 300
 Oy 61 CTGGAAGAAACACATATAAAGACGATATGCTTTCTCTATTAAGAAAGGATGCTCT 120
 Db 301 CTGGAAGAAACACATATAAAGACGATATGCTTTCTCTATTAAGAAAGGATGCTCT 360
 Oy 121 GTAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
 Db 361 GTAAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Oy 181 GAAACCTTTGTGCTGCTGCTTCCAGTCACCTACACCGCTGTCAAGACCTTGTGATGTC 240

Db 421 GAGCCCTTTGGTCTGGTCAATCTCCACACATGCTGTCAGAGACTTGGTGAATATC 480
Qy 241 CCCGTGCACACACCCCTGAGACATCCGTTAGAGAGATGATGAGCTGGCTGATGCTTAC 300
Db 481 CCCGTGCACACACCCCTGAGACATCCGTTAGAGAGATGATGAGCTGGCTGATGCTTAC 540
Qy 301 ACAGATGTGAACGTCGCTGGAATCAGAGATTTTCATTTTCATGGGTGACTTCAATGCT 360
Db 541 ACGGACGTGAACACACCGCTGGAAGCGGAGAAATTTTCATTTTCATGGGTGACTTCAATGCC 600
Qy 361 GGCTCAGCTACGTCCTCCCAAGAGCCCTGGAAGGACATCCGCTGAGGACGAGACCCCAAG 420
Db 601 GGCTCAGCTACGTCCTCCCAAGAGCCCTGGAAGGACATCCGCTGAGGACGAGACCCCAAG 660
Qy 421 TTGCTTTGGCTGATCGGGGACCAAGAGGACACCGGTCAAGAGAGACCAAACTGGGCC 480
Db 661 TTGCTTTGGCTGATCGGGGACCAAGAGGACACCGGTCAAGAGAGACCAAACTGGTGA 720
Qy 481 TATGACAGGATCGCTGATAGGAGCAAAATTTGTCAACTCTGGTGGTCTCAATCAATCAAC 540
Db 721 TATGACAGGATCGCTGATAGGAGCAAAATTTGTCAACTCTGGTGGTCTCAATCAATCAAC 780
Qy 541 CTCGCTTTGATTTCCAGAAAGCTTACAGGTTGTCGAATCGAAGGCCCTCGG 592
Db 781 AGTGTGTTGACTTCCAGAAAGCTTACAGGTTGTCGAATCGAAGGCCCTCGG 832

RESULT 6
US-10-133-065-1
; Sequence 1, Application US/10133065
; Patent No. US20020123122A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; Baron, Will F.
; TITLE OF INVENTION: HUMAN DNASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/133,065
; FILING DATE: 26-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/643,520
; FILING DATE: 22/08/2000
; APPLICATION NUMBER: 08/794827
; FILING DATE: 04-Feb-1997
; APPLICATION NUMBER: 60/109796
; FILING DATE: 05-Feb-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W
; REGISTRATION NUMBER: *See attached Limited Recognition under 37
; REFERENCE/DOCKET NUMBER: C.F.R. 10.9(b)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single

; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-133-065-1
Query Match 80.5%; Score 476.8; DB 12; Length 1079;
Best Local Similarity 87.8%; Pred No. 3.2e-140;
Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
Qy 1 GAGAAGCTAAACGGAAATTCAGAAAGAGGATACATACATCAATATGTGATTAGCTCTCGC 60
Db 287 GAGAAGCTGAACGAAATTCAGAGAGAGGATACATACATCAATATGTGATTAGCTCTCGC 346
Qy 61 CTTGGAAGAAACACATATAAAGACATATGCTTTCTTATAAAGAAAGCTAGTGTCT 120
Db 347 CTTGGAAGAAACACATATAAAGACATATGCTTTCTTATAAAGAAAGCTAGTGTCT 406
Qy 121 GTAACAAAGAGTACCTCTACACGACTATCAGGCTGGAGACGAGATGTGTTTCCAGG 180
Db 407 GTGAGAGAGGAGTTATCACTACCATGATATCAGATGAGACGAGATGTGTTTCCAGG 466
Qy 181 GAACCCCTTTGGTCTGGTTCAGTCCAGTACACCTTACACCGCTGTCAAGGACTTCGTGATTGC 240
Db 467 GAGCCCTTTGGTCTGGTTCAGTCCAGTACACCTTACACCGCTGTCAAGGACTTCGTGATTGC 526
Qy 241 CCCCTGCACACACCCCTGAGACATCCGTTAGAGAGATGATGAGCTGGCTGATGCTTAC 300
Db 527 CCCCTGCACACACCCCTGAGACATCCGTTAGAGAGATGATGAGCTGGCTGATGCTTAC 586
Qy 301 ACAGATGTGAACCGTCTCGTGGATGACAGAGATTTTCATTTTCATGGGTGACTTCAATGCT 360
Db 587 ACGGACGTGAACACACCGCTGGAAGCGGAGAAATTTTCATTTTCATGGGTGACTTCAATGCC 646
Qy 361 GGCTGACGACTACGTCCTCCCAAGAGGCTGGAAGGACATCCGCTGAGGACGAGACCCCAAG 420
Db 647 GGCTGACGACTACGTCCTCCCAAGAGGCTGGAAGGACATCCGCTGAGGACTGACCCCAAG 706
Qy 421 TTGCTTTGGCTGATCGGGGACCAAGAGGACACCGGTCAAGAGAGACCAAACTGGGCC 480
Db 707 TTGCTTTGGCTGATCGGGGACCAAGAGGACACCGGTCAAGAGAGACCAAACTGGTGA 766
Qy 481 TATGACAGGATCGTGTCTTAGAGGACCAAAATTTGTCAACTCTGGTGGTCTCAATCAATCAAC 540
Db 767 TATGACAGGATCGTGTCTTAGAGGACCAAAATTTGTCAACTCTGGTGGTCTCAATCAATCAAC 826
Qy 541 CTGCTCTTTGATTTCCAGAAAGCTTACAGGTTGTCGAATCGAAGGCCCTCGG 592
Db 827 AGTGTGTTTGAATTTCCAGAAAGCTTACAGTGAAGAGGAGGCCCTCGG 878
RESULT 7
US-10-074-509-1
; Sequence 1, Application US/10074509
; Patent No. US20020142437A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; Baron, Will F.
; TITLE OF INVENTION: HUMAN DNASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/074,509
; FILING DATE: 11-Feb-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/643,520
FILING DATE: 22/08/2000
APPLICATION NUMBER: 08/794827
FILING DATE: 04-Feb-1997
APPLICATION NUMBER: 60/109796
FILING DATE: 05-Feb-1996
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: P1000R1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3562
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-074-509-1
Query Match 80.5%; Score 476.8; DB 12; Length 1079;
Best Local Similarity 87.8%; Pred. No. 3.2e-140;
Matches 520; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 1 GAGAGCTAAACGGAATTCAAGAAAGGACATACATACATATGATTAGCTCTCGC 60
DB 287 GAGAACTGAACGAAATTCAGAGAGGCGATACGACAACTATGTGATTAGCTCTCGC 346
QY 61 CTTGSAAGAAACATATTAAGAAAGATAGCTTTCTCTATTAAGAAAGATAGTCT 120
DB 347 CTTGSAAGAAACATATTAAGAAAGATAGCTTTCTCTATTAAGAAAGATAGTCT 406
QY 121 GTAAAAAAGACTACCTCTACACGACTATCAGCTGAGAGCAGATGTTTCCAG 180
DB 407 GTGAAGAGAGTTATCATCTACATGACTATCAGATGAGAGCCGATGTGTTTCCAG 466
QY 181 GAACCTTTGTGTGCTGTTCAGTCACTTACACCGCTGTCAAGACATTGATTGTC 240
DB 467 GAGCCCTTTGTGTGCTGTTCAGTCACTTACACCGCTGTCAAGACATTGATTGTC 526
QY 241 CCCCTGACACACCCCTGAGATCCGTTAGAGATGATGAGCTGCTGATGCTTAC 300
DB 527 CCCCTGACACACCCCTGAGATCCGTTAGAGATGATGAGCTGCTGATGCTTAC 586
QY 301 ACAGATGTGAACGTCGTGGAATGAGAGATTTTCAATTTTCAATGCTCAATGCT 360
DB 587 ACAGATGTGAACGTCGTGGAATGAGAGATTTTCAATTTTCAATGCTCAATGCT 646
QY 361 GCGTGAAGTACGTCCTCCCAAGAGCCCTGAGAGACATCCGCTGAGAGACCCCAAG 420
DB 647 GCGTGAAGTACGTCCTCCCAAGAGCCCTGAGAGACATCCGCTGAGAGACCCCAAG 706
QY 421 TTGCTTTGCTGATCGGGGACCAAGAGACACACGCTGACGAAGAGCAAAATGCGCC 480
DB 707 TTGCTTTGCTGATCGGGGACCAAGAGACACACGCTGACGAAGAGCAAAATGCGCC 766
QY 481 TATGACAGATCGTGTGAGAGACAAATATTTCACTCTGCTGCTCTCATCAAC 540
DB 767 TATGACAGATCGTGTGAGAGACAAATATTTCACTCTGCTGCTCTCATCAAC 826
QY 541 CTCGCTTTGATTTCAGAAAGCTTACAGGTTGCTGAATGAGAGCCCTG 592
DB 827 AGTGTTTTCAGCTTCCAGAAAGCTTACAGGTTGCTGAATGAGAGCCCTG 878

RESULT 9
US-10-133-065-11
; Sequence 11, Application US/10133065
; Patent No. US20020123122A1

GENERAL INFORMATION:
APPLICANT: Baron, Kevin P.
TITLE OF INVENTION: HUMAN DNASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/133,065
FILING DATE: 26-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/643,520
FILING DATE: 22/08/2000
APPLICATION NUMBER: 08/794827
FILING DATE: 04-Feb-1997
APPLICATION NUMBER: 60/109796
FILING DATE: 05-Feb-1996
ATTORNEY/AGENT INFORMATION:
NAME: Evans, David W
REGISTRATION NUMBER: C.F.R. 10.9(b)
REFERENCE/DOCKET NUMBER: *See attached Limited Recognition under 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1739
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1124 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-133-065-11
Query Match 73.5%; Score 435.2; DB 12; Length 1124;
Best Local Similarity 83.4%; Pred. No. 4.2e-127;
Matches 494; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 1 GAGAGCTAAACGGAATTCAAGAAAGGACATACATACATATGATTAGCTCTCGC 60
DB 404 GAGAGCTGAATGAAATTCAGAAAGGACACAACTATGATTAGCTCTCGA 463
QY 61 CTTGSAAGAAACATATTAAGAAAGATAGCTTTCTCTATTAAGAAAGATAGTCT 120
DB 464 CTTGSAAGAAACATATTAAGAAAGATAGCTTTCTCTATTAAGAAAGATAGTCT 523
QY 121 GTAAAAAAGACTACCTCTACACGACTATCAGCTGAGAGCCGATGTTTCCAG 180
DB 524 GTGAAGAGAGTTATCATCTACATGACTATCAGATGAGAGACACACGCTTTCCAG 583
QY 181 GAACCTTTGTGTGCTGTTCAGTCACTTACACCGCTGTCAAGACATTGATTGTC 240
DB 584 GAGCCCTTTGTGTGCTGTTCAGTCACTTACACCGCTGTCAAGACATTGATTGTC 643
QY 241 CCCCTGACACACCCCTGAGATCCGTTAGAGATGATGAGCTGCTGATGCTTAC 300
DB 644 CCCCTGACACACCCCTGAGATCCGTTAGAGATGATGAGCTGCTGATGCTTAC 703
QY 301 ACAGATGTGAACGTCGTGGAATGAGAGATTTTCAATTTTCAATGCTCAATGCT 360
DB 704 ACAGATGTGAACGTCGTGGAATGAGAGATTTTCAATTTTCAATGCTCAATGCT 763

Query Match	Score	DB 12;	Length
Best Local Similarity	83.4%;	Pred. No. 4,2e-127;	
Matches :494;	Conservative	0; Mismatches 98;	Indels 0; Gaps
Qy	1	GAGAAAGCTAAACGGAAATTC	CAAGAAAGGCGATACATACAACTATGTGATTAGCTTCGC 60
ph:	404	GAGAAAGCTGATGGAAATTC	GAGAAAGAGACACATACAACTATGTGATTAGCTTCGA 463

	Query Match	29.0%	Score 171.4;	DB 10;	Length 392;
	Best Local Similarity	86.0%;	Pred. No. 2.8e-44;		
	Matches 190;	Conservative	0;	Mismatches 31;	Indels 0;
	Gaps				
QY	372	CGTCCCAAGAGCGCTGGGAAGGACATCCGCTGAGACGCGACCCCAAGTTCGTTTGGCT	4311		
Db	392	CGTCCCAAGAGCGCTGGGAAGGACATCCGCTGAGACGCGACCCCAAGTTCGTTTGGCT	3333		
QY	432	GATCGGGGACCAAGAGGACACACCGTCAAGAAGAGACAAACTCGCCCTATGACAGGAT	4911		

Db 332 GATCGGGGACCAAGAGACACCGGTGAAGAGAGACCAACTGTGCATATGACAGGAT 273
Qy 492 CGTGCTTAGAGGACAAATATTTCAACTCTGCTGCTCTCAATCAAACTCTCTTTGA 551
Db 272 TGTGCTTAGAGGACAAAGAACTGTCTGTTGTTCCCAAGTCAACAGTGTTTGA 213
Qy 552 TTTCAGAAAGCTTACAGGTTGTCTGAATGAAGGCCCTGG 592
Db 212 CTTCCAGAAAGCTTACAAGCTGACTGAAAAGGAGGCCCTGG 172

RESULT 11

US-09-771-078-1
; Sequence 1, Application US/09771078
; Patent No. US20020034727A1
; GENERAL INFORMATION:
; APPLICANT: Mreny, Randall J.,
; APPLICANT: Daugherty, Ann L.,
; APPLICANT: Patapoff, Thomas W.
; TITLE OF INVENTION: DNase Compaction Assay
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/771,078
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/971,019
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J.
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: 792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3177
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1039 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-771-078-1

Query Match 25.2%; Score 149.4; DB 10; Length 1039;
Best Local Similarity 56.7%; Pred. No. 4.1e-37;
Matches 317; Conservative 0; Mismatches 236; Indels 6; Gaps 2;
Qy 34 ACATACAACTATGTGATTAGCTCTCGCCCTTGGAAAGAAACACATATAAAGAACAGTATGCC 93
Db 409 ACCTATCACTACGTGTGCTAGTGAGCCACTGGGACGAAACAGCTATAAGGAGCGCTACCTG 468
Qy 94 TTTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACTCTTACCAGCA---CTAT 150
Db 469 TTCGTGTACAGGCTGACCAAGTGTCTGCGGTGGACAGCTACTACTACGATGATGCTGC 528
Qy 151 CAGGCTGGAGACGACAGTGTCTTCCAGGGAACCTTTGTGGTCTGCTTCCAGTCAACCC 210
Db 529 GAGCCCTGGGGAACGACACCTTCAACCGAGAGCCAGCCATTGTGAGGTTCTTCTCCCGG 588

Qy 211 TACACCGCTGTCAAGACTTCTGTGATTGTCCCTTCGCACACCACTCTGAGACATCCGTT 270
Db 589 TACACAGAGGTCAAGGAGTTTGCATTGTTCCTTCATCGCGCCCGGGGAGCAGTA 648
Qy 271 AGAGAGATTGATGAGCTGGCTGATGTACACAGATGTGAACGTCGCTGGAATGCAGAG 330
Db 649 GCGGAGATCGAGCTCTCTATGACGCTACTCTGATGTCCAAGAGAAATGGGCGCTGGAG 708
Qy 331 AATTTTCATTTTCATGGGTGACTTCAATGTGCTGCTGAGCTACGTCCCAAGAGGCGCTGG 390
Db 709 GAGCTCATGTTGATGGCGACTTCAATGCGGCTGCTGAGCTATGTGAGACCTCCAGTGG 768
Qy 391 AAGGACATCCGCTGAGGACGACCCCAAGTTGCTTTGGCTGATCGGGGACCAAGAGGAC 450
Db 769 TCATCCATCCGCTGTGGACAAGCCCACTTCCAGTGGCTGATCCCCGACAGCGCTGAC 828
Qy 451 ACCAGGTCAAGAAGAGACAAACTCGCGCTATGACAGGATCGTCTTAGAGGACAAAAT 510
Db 829 ACCACAG---CTACCCACGCACTGTGCTATGACAGGATCGTGTTCAGGGATGCTG 885
Qy 511 ATTGTCAACTCTGGTGTCTCTCAATCAAACTCTCGTCTTTGATTTCCAGAAAGCTTACAGG 570
Db 886 CTCGAGGCGCGTGTGTTCCGCACTCGGCTCTCCCTTTAACTTCCAGGCTGCTATGGC 945
Qy 571 TTGCTCTGAATCGAAGGCC 589
Db 946 CTGAGTGACCAACTGGCCC 964

RESULT 12

US-09-825-012-2
; Sequence 2, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1039
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-825-012-2

Query Match 25.2%; Score 149.4; DB 10; Length 1039;
Best Local Similarity 56.7%; Pred. No. 4.1e-37;
Matches 317; Conservative 0; Mismatches 236; Indels 6; Gaps 2;
Qy 34 ACATACAACTATGTGATTAGCTCTCGCCCTTGGAAAGAAACACATATAAAGAACAGTATGCC 93
Db 409 ACCTATCACTACGTGTGCTAGTGAGCCACTGGGACGAAACAGCTATAAGGAGCGCTACCTG 468
Qy 94 TTTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACTCTTACCAGCA---CTAT 150
Db 469 TTCGTGTACAGGCTGACCAAGTGTCTGCGGTGGACAGCTACTACTACGATGATGCTGC 528
Qy 151 CAGGCTGGAGACGACAGTGTGTTTCCAGGGAACCTTTGTGGTCTGCTTCCAGTCAACCC 210
Db 529 GAGCCCTGGGGAACGACACCTTCAACCGAGAGCCAGCCATTGTGAGGTTCTTCTCCCGG 588
Qy 211 TACACCGCTGTCAAGACTTCTGTGATTGTCCCTTCGCACACCACTCTGAGACATCCGTT 270
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Qy 271 AGAGAGATTGATGAGCTGGCTGATGTCTACAGATGTGAACGCTGCTGGAATGCAGAG 330

Db 649 GCCGAGTCAGCGCTCTCTATGACGTCTACCTGATGTCACCAAGAAATGGGGCTTTGGAG 708
Qy 331 AATTTCATTTTCATGAGTACTTCAATGCTGTGCGTGCAGCTACGCTCCCAAGAAAGGCTTGG 390
Db 709 GACGTCATGTTGATGGGCGACATTTCAATGCGGGCTGCGAGCTATGTGAGACCTTCCCACTGG 768
Qy 331 AAGGACATCCGCTGAGAGCGGACCCCAAGTTCGTTTGGCTCATCGGGGACCAAGAGAC 450
Db 769 TCATCCATCCGCTGTGAGCAAGCCCCCAGCTTCAGTGTCTATCCCGACGCGCTGAC 828
Qy 451 ACCAGGTCAGAAAGAGCAAACTGCGCTATGACAGAGTGTGCTTGAAGACAAAT 510
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Qy 511 ATTGTCAACTGTGTGCTTCAATCAAACTGCTTTGATTTCCAGAAAGCTTACAG 570
Db 886 CTCGAGGCGCGCTGTGCTCCGACCTGCGCTTCCCTTTAACTTCAGGCTGCTATGGC 945
Qy 571 TTGTCTGAATGGAAGGCC 589
Db 946 CTGAGTGAACCAACTGGCCC 964

RESULT 13

US-09-825-012-4
; Sequence 4, Application US/09825012
; Patent No. US2002012798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-012-4

Query Match 25.0%; Score 147.8; DB 10; Length 783;
Best Local Similarity 56.5%; Pred. No. 1.1e-36;
Matches 316; Conservative 0; Mismatches 237; Indels 6; Gaps 2;

Qy 34 ACATCAACTATGTGATTAGCTCTGCGCTTGGAGAAACACATATTAAGAAAGATATGCC 93
Db 184 ACCTATCACTACGTGTGAGAGGCGACCTGGAGCGAAACGCTATTAAGAGGCTTACCTG 243
Qy 94 TTTCTCTAATAAGAAAGCTAGTGTCTGTAAACAAGTACTACTTACACAGA---CTAT 150
Db 244 TTCGTGTACAGGCGCTGACAGGTGTCTGCGGTGACAGTACTACTATGATATGGCTGC 303
Qy 151 CAGGCTGAGAGCGAGATGTGTTTCCAGGGAACTTTGTGTTGTTCCAGTACCC 210
Db 304 GAGCCCTCGGGAAAGACACCTTCAACGAGAGCCAGCATGTGAGGTTCTTCCCGG 363
Qy 211 TACACCGCTGTCAAGAGACTTGTGATTTGCCCTGACACACACCCCTGAGACATCCGT 270
Db 364 TTCACAGAGGTGAGGAAATTTGCAATTTTCCCTGCAATGCGGCCCGGGGAGCGCAATA 423
Qy 271 AGAGAGATTGATGAGCTGGCTGATCTTCAACAGATGTGAAGAGTCCGCTGAAATGCAAG 330
Db 424 GCCGAGTCAGAGCTCTCTATGACGTCTTACCTGAGATGTCCAAAGAAATGGGGCTTGAAG 483
Qy 331 AATTTCATTTTCATGAGTACTTCAATGCTGTGCTGACGCTCCCAAGAAAGGCTTGG 390
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Qy 331 AAGGACATCCGCTGAGAGCGAGCCCAAGTTCGTTTGGCTGATCGGGACCAAGAGAC 450
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Qy 451 ACCAGGTCAGAAAGAGCAAACTGCGCTATGACAGAGTGTGCTTGAAGACAAAT 510
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Qy 571 TTGTCTGAATGGAAGGCC 589
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RESULT 14

US-09-825-012-6
; Sequence 6, Application US/09825012
; Patent No. US2002012798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-012-6

Query Match 25.0%; Score 147.8; DB 10; Length 858;
Best Local Similarity 56.5%; Pred. No. 1.2e-36;
Matches 316; Conservative 0; Mismatches 237; Indels 6; Gaps 2;

Qy 34 ACATCAACTATGTGATTAGCTCTGCGCTTGGAGAAACACATATTAAGAAAGATATGCC 93
Db 259 ACCTATCACTACGTGTGAGAGGCGACCTGGAGCGAAACGCTATTAAGAGGCTTACCTG 318
Qy 94 TTTCTCTAATAAGAAAGCTAGTGTCTGTAAACAAGTACTACTTACACAGA---CTAT 150
Db 319 TTCGTGTACAGGCGCTGACAGGTGTCTGCGGTGACAGTACTACTATGATATGGCTGC 378
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Db 379 GAGCCCTCGGGAAAGACACCTTCAACGAGAGCGAGCATGTGAGGTTCTTCCCGG 438
Qy 211 TACACCGCTGTCAAGAGACTTGTGATTTGCCCTGACACACCCCTGAGACATCCGT 270
Db 439 TTCACAGAGGTGAGGAAATTTGCAATTTTCCCTGATGTGCGGCCCGGGGAGCGCAATA 498
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Qy 331 AATTTCATTTTCATGAGTACTTCAATGCTGTGCTGACGCTCCCAAGAAAGGCTTGG 390
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Qy 451 ACCAGGTCAGAAAGAGCAAACTGCGCTATGACAGAGTGTGCTTGAAGAGCAAAAT 510

Db 679 ACCACAG---CTACACCCAGCAGCTGTGCTATGACAGGATCGTGTTCAGGGATGCTG 735
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RESULT 15

US-09-825-012-62
; Sequence 62, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMPG1 Fd - DNase I fusion
US-09-825-012-62

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Best Local Similarity 56.5%; Pred. No. 1.7e-36;
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QY 34 ACATACAACGTATGTATTAGTCTCGCCTTGAAGAAACACATATAAAGAACAGTATGCC 93
Db 949 ACCTATCACTAGTGTGCTAGTGAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTG 1008
QY 94 TTTCTCTATAAAAGAAAGCTAGTGTCTGTAAACAAAGCTACCTCTACCACGA---CTAT 150
Db 1009 TTGCGGTACAGCCCTGACCAGGTGCTCGGTGGACAGCTACTACTACGATGATGCTGC 1068
QY 151 CAGGCTGGAGACGAGATGTGTTTCCAGGGAAACCTTTTGTGGTCTGTGTTCCAGTCACCC 210
Db 1069 GAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATTGTGAGGTTCTTCTCCCGG 1128
QY 211 TACACCGCTGTCAAGACTTCGTGATTGTCGCCCTGCACACCCCTGAGACATCCGTT 270
Db 1129 TTCACAGAGTTCAGGAGTTTGCCTATTGTTCCCTGTCATGCGGCCCGGGGACGAGTA 1188
QY 271 AGAGAGATTGATGAGCTGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAG 330
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Db 1249 GACGTCATGTTGATGGGACCTTCAATGCGGCTGAGCTATGTGAGACCTCCAGTGG 1308
QY 391 AAGGACATCCGCTGAGGACGACCCCAAGTTTCGTTGGCTGATCGGGACCAAGAGGAC 450
Db 1309 TCATCCATCCGCTGTGGACAAAGCCCCACCTTCCAGTGGCTGATCCCCACACGCGCTGAC 1368
QY 451 ACCACGGTCAAGAAGAGCACAACCTGCGCTATGACAGGATCGTGTAGAGACAAAAAT 510
Db 1369 ACCACAG---CTACACCCACGCACTGTGCTATGACAGGATCGTGGTTCAGGGATGCTG 1425
QY 511 ATGTCAACTCTGGTGGTCTCAATCAAAACCTCGTCTTTTGATTTCAGAAAGCTTACAGG 570

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QY 571 TTGTCCTGAATCGAAGGCC 589
Db 1486 CTGAGTGACCAACTGGCCC 1504
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Job time : 127.65 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Perfect score: 671
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Gapop 10_0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 40: em_hugo_mus.*
- 41: em_hugo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	527	78.5	1023	6	AX329742	AX329742 Sequence
2	527	78.5	1023	6	AX332286	AX332286 Sequence
3	527	78.5	1023	6	AX332789	AX332789 Sequence
4	527	78.5	1023	6	AX410746	AX410746 Sequence
5	527	78.5	1023	6	HSU56814	U56814 Human DNase
6	527	78.5	1067	9	BC015831	BC015831 Homo sapi
7	527	78.5	1079	9	AF047354	AF047354 Homo sapi
8	525.4	78.3	1108	9	HSU75744	U75744 Homo sapien
9	501.4	74.7	1331	10	AF039852	AF039852 Rattus norv
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17	298.4	44.5	1250	5	AF059612	AF059612 Xenopus l
18	195.6	29.2	392	6	AX330074	AX330074 Sequence
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24	164.8	24.6	1161	4	D82875	D82875 Oryctolagus
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39	161.6	24.1	1554	6	AX268702	AX268702 Sequence
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LOCUS	Sequence 251 from Patent WO0194629.					
DEFINITION	AX329742					
ACCESSION	AX329742					
VERSION	AX329742.1	GI:18102720				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,					
	Horrigan, S., Soppet, D.R. and Weaver, Z.					
TITLE	Cancer gene determination and therapeutic screening using signature					

Gene sets
Patent: WO 0194629-A 251.13-DEC-2001;
Avalon Pharmaceuticals (US)

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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 312 a 244 c 240 g 227 t
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Query Match 78.5%; Score 527; DB 6; Length 1023;
Best Local Similarity 87.8%; Pred. No. 1.1e-132;
Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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RESULT 2
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LOCUS AX332286
DEFINITION Sequence 2795 from Patent WO0194629.
ACCESSION AX332286
VERSION AX332286.1 GI:18122920
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrikan, S., Sopet, D. R. and Weaver, Z.

TITLE Cancer gene determination and therapeutic screening using signature

JOURNAL
Patent: WO 0194629-A 2795.13-DEC-2001;
Avalon Pharmaceuticals (US)

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 312 a 244 c 240 g 227 t
ORIGIN

Query Match 78.5%; Score 527; DB 6; Length 1023;
Best Local Similarity 87.8%; Pred. No. 1.1e-132;
Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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QY 61 CATACACTATGTGATTAAGCTCTGCTGCTGGAAGAAACATATAAGACAGTATGCT 120
DB 275 CATACACTATGTGATTAAGCTCTGCTGCTGGAAGAAACATATAAGACAGTATGCT 334
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DB 815 CTGAATCGAAGGCCCTGATGTCAGCGACCACTTCCAGTTCAATCATCATCATCA 869
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RESULT 3
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LOCUS AX332789
DEFINITION Sequence 3298 from Patent WO0194629.
ACCESSION AX332789
VERSION AX332789.1 GI:18123423
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,

[illegible]

AUTHORS Rodriguez, A.M., Rodin, D., Nomura, H., Morton, C.C., Weremowicz, S. and Schneider, M.C.
TITLE Identification, localization, and expression of two novel human genes similar to deoxyribonuclease I
JOURNAL Genomics 42 (3), 507-513 (1997)
MEDLINE 97349121
PUBMED 9205125
REFERENCE 2 (bases 1 to 1023)
AUTHORS Schneider, M.C. and Rodriguez, A.
JOURNAL Direct Submission
 Submitted (25-APR-1996) M.C. Schneider, Renal Division, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115, USA
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 DQEDTTVKSTNCAYDRIVLRGQEIIVSVPKNSVDFQKAYKLTLEEDLVSDHFP
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 BASE COUNT 312 a 244 c 240 g 227 t
 ORIGIN

Query Match 78.5%; Score 527; DB 9; Length 1023;
 Best Local Similarity 87.8%; Pred. No. 1,1e-132;
 Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1 ACAACAGATCTGCCCTACTGATGAGAGAACTAAACGAAATTCAGAAAGGCATTA 60
 DB 215 ACAACAGATCTGCCCTACTGATGAGAGAACTAAACGAAATTCAGAAAGGCATTA 274
 QY 61 CATACACTATGTGATGATCTCCCTTGAAGAAACATATTAAGAACATATGCTT 120
 DB 275 CGTACAATATGTGATGATCTCCCTTGAAGAAACATATTAAGAACATATGCTT 334
 QY 121 TTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACTACCAAGCATATCAGG 180
 DB 335 TTCTCTATAAGAAAGCTAGTGTCTGTAAAGAGATTATCATCACTATCAGG 394
 QY 181 CTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 395 ATGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 454
 QY 241 CCGGCTCAAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 DB 455 CTGCTGTAAAGACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 514
 QY 301 AGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 515 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
 QY 361 TCATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 575 TCATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 634
 QY 421 ACATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 635 ACATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 694

QY 481 CGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 695 CGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 754
 QY 541 TCAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 755 TCAACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 814
 QY 601 CTGAATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 655
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RESULT 6
 BC015831
 LOCUS
 DEFINITION Homo sapiens, deoxyribonuclease I-like 3, clone MGC:27146
 IMAGE:4723725, mRNA, complete cds.
 ACCESSION BC015831
 VERSION BC015831.1 GI:16198370
 KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
 1 (bases 1 to 1067)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gcaps-remail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLML)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadnan@systemsbio.org
 Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Ketterman and Anuradha Madan

FEATURES
 source
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 /db_xref="LocusID:1776"
 /db_xref="taxon:9606"
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 VEFKLOSRAFTNSKSVTLRKTKSKRS"
 BASE COUNT 327 a 256 c 249 g 235 t
 ORIGIN

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLML at: <http://image.lnl.gov>
 Series: IRAL Plate: 38 Row: P Column: 7
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 4826697.

Query Match		78.5%; Score 527; DB 9; Length 1067;
Best Local Similarity		87.8%; Pred. No. 1.1e-132;
Matches 575; Conservative		0; Mismatches 80; Indels 0; Gaps 0;
QY	1	ACACAGGATCTGCCCATCTGATGAGAGCTAAACCGAAATTCAGAAAGGCGATAA 60
	258	ACAACAGGATCTGCCCATCTGATGAGAGCTGACAGAAATTCAGAGAGGCGATAA 317
QY	61	CATACAACTATGTGATTAGCTCTCGCTTGGAGAGAACACATATAAGAACAGTATGCCT 120
Db	318	CGTACAACTATGTGATTAGCTCTCGCTTGGAGAGAACACATATAAGAACATATGCCT 377
QY	121	TTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACCTCTACCGAGCTATCAGG 180
Db	378	TTCTCTACAAAGAAAGCTGGTGTCTGTGAAGAGGAGTTATCACTACCATGACTATCAGG 437
QY	181	CTGGAGACGAGATGTGTTTCCAGGGAACCTTTGTGTCTGTTCCAGTACCCCTACA 240
Db	438	ATGGAGACGAGATGTGTTTCCAGGAGCCCTTTGTGTCTGTTCCCAATCTCCCCACA 497
QY	241	CGCTCTCAAGGACTTCGTGATTGTCCTCCCTGCACACACCCCTGAGACATCCGTTAGAG 300
Db	498	CTGCTGTCAAGACTTCGTGATTATCCCTCTGCACACACCCCGAGAGATCCGTTAAGG 557
QY	301	AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAACGTCGCTGGAATGCAGAAATT 360
Db	558	AGATCGATGAGTTGGTTGAGGTCTACACGAGCTGAAACACCGCTGAGAGCGGAGAAAT 617
QY	361	TCAATTTTCATGGTGACTTCAATCTGGCTGACGCTACGTCGCCCAAGAGGCTTGAAGG 420
Db	618	TCAATTTTCATGGTGACTTCAATCTGGCTGACGCTACGTCGCCCAAGAGGCTTGAAGA 677
QY	421	ACATCCGCTGAGGACCGACCCCAAGTTCGTTGGCTGATCGGGACCAAGAGGACACCA 480
Db	678	ACATCCGCTGAGGACGACCCCAAGTTCGTTGGCTGATCGGGACCAAGAGGACACCA 737
QY	481	CGGTCAAGAGAGCAAACTGCGCCTATGACAGGATCGTGTCTAGAGGACAAAATATTG 540
Db	738	CGGTGAAGAGAGCAAACTGTGCATATGACAGGATTCGCTTAGAGGACCAAGAAATCG 797
QY	541	TCACTCTGGTGTCTCAATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGTTGT 600
Db	798	TCAGTTCTGTGTTCCCAAGTCAAAACAGTGTGTTTTCAGTTCCAGAAAGCTTACAAGCTGA 857
QY	601	CTGAATCGAAGGCCCTGGATGTCAGGACCACTTTCCAGTTCATCATCATCA 655
Db	858	CTGAAGAGGAGGCCCTGGATGTCAGGACCACTTTCCAGTTCATCATCATCA 912
RESULT 7		
LOCUS		AF047354
DEFINITION		Homo sapiens liver and spleen DNase precursor (LSD) mRNA, complete cds.
ACCESSION		AF047354
KEYWORDS		AF047354.1 GI:2905785
SOURCE		Homo sapiens.
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		Baron, W.F., Pan, C.Q., Spencer, S.A., Ryan, A.M., Lazarus, R.A. and Baker, K.P.
TITLE		Cloning and characterization of an actin-resistant DNase I-like endonuclease secreted by macrophages
JOURNAL		Gene 215 (2), 291-301 (1998)
MEDLINE		9838252
PUBMED		9714828
REFERENCE		2 (bases 1 to 1079)
AUTHORS		Baron, W.F., Pan, C.Q., Spencer, S.A., Ryan, A.M., Lazarus, R.A. and Baker, K.P.
Direct Submission		
Submitted (09-FEB-1998)		Molecular Biology, Genentech Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES		Location/Qualifiers
source		1..1079
gene		/organism="Homo sapiens" /db_xref="taxon:9606"
CDS		1..1079 /gene="LSD" 71..988 /gene="LSD" /note="actin resistant activity; macrophage specific DNase I; LS-DNase" /codon_start=1 /product="liver and spleen DNase precursor" /protein_id="AAC35752.1" /db_xref="GI:2905786"
sig_peptide		71..130 /gene="LSD" /evidence=experimental
mat_peptide		131..985 /gene="LSD" /product="liver and spleen DNase"
BASE COUNT		330 a 260 c 252 g 237 t
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Query Match		78.5%; Score 527; DB 9; Length 1079;
Best Local Similarity		87.8%; Pred. No. 1.1e-132;
Matches 575; Conservative		0; Mismatches 80; Indels 0; Gaps 0;
QY	1	ACAACAGGATCTGCCCATCTGATGAGAGCTAAACCGAAATTCAGAAAGGCGATAA 60
Db	261	ACAACAGGATCTGCCCATCTGATGAGAGCTGAACAGAAATTCAGAGGAGGCGATAA 320
QY	61	CATACAACTATGTGATTAGCTCTCGCTTGGAGAGAACACATATAAGAACAGTATGCCT 120
Db	321	CGTCAACTATGTGATTAGCTCTCGCTTGGAGAGAACACATATAAGAACAAATATGCCT 380
QY	121	TTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACCTCTACCGAGCTATCAGG 180
Db	381	TTCTCTACAGAAAGCTGGTGTCTGTGAAGAGGAGTTATCACTACCATGACTATCAGG 440
QY	181	CTGGAGACGCGAGATGTGTTTCCAGGGAACCCCTTTGTGGTTCGCTTCCAGTCAACCTTACA 240
Db	441	ATGGAGACGCGAGATGTGTTTCCAGGAGCCCTTTGTGTCTGTTCCAATCTCCCCACA 500
QY	241	CGCTGTCAAGAGACTTCGTGATTGTCCTCCCTGACACACCCCTTGAGACATCCGTTAGAG 300
Db	501	CTGCTGTCAAGAGACTTCGTGATTATCCCTCTGCACACCCCTGAGAGACATCCGTTAAGG 560
QY	301	AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAACGCTCGCTGGAATGCAGAGAAAT 360
Db	561	AGATCGATGAGTTGGTTGAGGTCTACCGAGCTGGAACACCGCTGGAGGCGCGAGAAAT 620
QY	361	TCATTTTCATGGTGACTTCAATGTGCTGCAGTCTGCTGCCCAAGAGGCTCGGAAGG 420
Db	621	TCATTTTCATGGTGACTTCAATGCCGCTGCAGTCTGCTCCCAAGAGGCTCGGAAGA 680
QY	421	ACATCCGCTGAGGAGCGGACCCCAAGTTGTTGCTGATCGGGACCAAGAGGACACCA 480
Db	681	ACATCCGCTTGAGGAGTCAACCCAGGTTGTTGCTGATCGGGACCAAGAGGACACCA 740
QY	481	CGGTCAAGAGAGCAAACTGCGCCTATGACAGGATCGTGTCTAGAGGACAAAATATTG 540
Db	741	CGGTGAAGAGAGCAAACTGTGATATGACAGGATTCGCTTAGAGGACAAAATATCG 800
QY	541	TCAACTCTGGTGGTCTCTCAATCAAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGT 600

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Db      801  TCAGTTCTGTTTCCCAAGTCAACAGTGTTCAGTTCAGAAAGTTCAAGCTGA 860
Qy      601  CTGAATCGAAGGCCCTGATGTCAGACCACTTCCAGTTCATCATCATCA 655
Db      861  CTGAAGAGAGAGCCCTGATGTCAGGACCACTTCCAGTTCATTAACACTACA 915

RESULT 8
HSU75744      1108 bp      mRNA      linear      PRI 17-JUN-1998.
LOCUS      HSU75744
DEFINITION      Homo sapiens DNase gamma mRNA, complete cds.
ACCESSION      U75744
VERSION      U75744.1 GI:3236319
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens.
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE      ShioKawa, D., Hiral, M. and Tanuma, S.
JOURNAL      CDNA cloning of human DNase gamma: chromosomal localization of its
REFERENCE      gene and enzymatic properties of recombinant protein
AUTHORS      Apoptosis 3 (2), 89-95 (1998)
JOURNAL      "2 (bases 1 to 1108)
AUTHORS      ShioKawa, D. and Tanuma, S.
TITLE      Direct Submission
JOURNAL      Submitted (23-OCT-1996) Biochemistry, Science Univ. of Tokyo,
FEATURES      Shinjuku-Ku Ichigaya Funagawaracho, Tokyo 162, Japan
SOURCE      Location/Qualifiers
1. 1108
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93. 1010
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/db_xref="GI:3236320"
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VEFKLOSRAFTNSKSVTLKTKTKSKS"
BASE COUNT      329 a 261 c 271 g 247 t
ORIGIN
Query Match      78.3%; Score 525.4; DB 9; Length 1108;
Best Local Similarity      87.6%; Pred. No. 3.1e-132;
Matches 574; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy      1  ACAAGAGATGCGCCCACTACTGATGAGAGCTAAACGAATTCAGAAAGGCATTA 60
Db      283  ACAAGAGATGCGCCCACTACTGATGAGAGCTAAACGAATTCAGAGAGGCATTA 342
Qy      61  CATACACTATGTGATTAAGCTCTCGCTTGAAGAAACAATATAAGAACATATGCTT 120
Db      343  CGTACACTATGTGATTAAGCTCTCGCTTGAAGAAACAATATAAGAACATATGCTT 402
Qy      121  TTCTTATAAAGAAAGCTAGTGTCTGTTAAACAAAGCTACTTACACGACTATGAG 180
Db      403  TTCTTATAAAGAAAGCTAGTGTCTGTTAAAGAGAGTATCATACATGACTATACAG 462
Qy      181  CTGAGAGCAGATGTTTTCACAGGAACCTTGTGTGTGTTCCAGTACCCCTACA 240
Db      463  ATGAGAGCAGATGTTTTCACAGGAACCTTGTGTGTGTTCCAGTATTCCTCCACA 522
Qy      241  CCGCTGTCAAGACTTCGTATTTGCCCTGACACACACCCCTGAGACATCCGTTAAG 300
Db      523  CTGCTGTCAAGACTTCGTATTTGCCCTGACACACACCCCTGAGACATCCGTTAAG 582

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Qy      301  AGATTGATGACCTGGCTGATGCTTACACAGATGTGAAACGTGCTGAAATGCAGAAATT 360
Db      583  AGATGATGATGATGTTGATGAGCTTACACAGAGCTGAAACACCGCTGGAAGCGGAGATT 642
Qy      361  TCATTTTATGAGGACTTCAATGCTGCTGACACTACGTCCTCCCAAGAGGCTTGAAAG 420
Db      643  TCATTTTATGAGGACTTCAATGCTGCTGACACTACGTCCTCCCAAGAGGCTTGAAAG 702
Qy      421  ACATCCGCTGAGAGACGACCCCAAGTTGTTGGCTGATGCGGAGACCAAGAGACACA 480
Db      703  ACATCCGCTGAGAGACTGACCCCAAGTTGTTGGCTGATGCGGAGACCAAGAGACACA 762
Qy      481  CGGTCAAGAGACACAAACTGCGCTTATGACAGAGATGTCCTTAGAGACAAATAATTG 540
Db      763  CGGTCAAGAGACACCAACTGCTCATATGACAGATGTCCTTAGAGACAAATAATG 822
Qy      541  TCAACTCTGCTGCTGCTCAATCAACAACTCGCTTGTGATTTCCAAAGCTTACAGGTTGT 600
Db      823  TCAGTTCTGTTTCCCAAGTCAACAGTGTGTTTGAAGCTTCCAGAAAGCTTACAGCTGA 882
Qy      601  CTGAATCGAAGGCCCTGATGTCAGACCACTTCCAGTTCATCATCATCATCA 655
Db      883  CTGAAGAGAGAGCCCTGATGTCAGACCACTTCCAGTTCATTAACACTACA 937

RESULT 9
AF039852      1331 bp      mRNA      linear      ROD 07-AUG-1998
LOCUS      AF039852
DEFINITION      Rattus norvegicus DNasey mRNA, complete cds.
ACCESSION      AF039852
VERSION      AF039852.1 GI:3395771
KEYWORDS
SOURCE      Rattus norvegicus.
ORGANISM      Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1331)
Lin, Q.Y., Pandey, S., Singh, R.K., Lin, W., Ribocco, M.,
Borow, Borowski, H., Smith, B., Leblanc, J., Walker, P.R. and
Sikorska, M.
DNasey: a rat DNaseI-like gene coding for a constitutively
expressed chromatin-bound endonuclease
Biochemistry 37 (28), 10134-10143 (1998)
9665719
PUBMED
2 (bases 1 to 1331)
Lin, Q.Y., Singh, R.K., Lin, W. and Sikorska, M.
Direct Submission
Submitted (24-DEC-1997) Institute for Biological Sciences, National
Research Council, 1200 Montreal Road, Bldg. M-54, Box 4, Ottawa, ON
K1A 0R6, Canada
FEATURES      Location/Qualifiers
1. 1331
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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153. 1085
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/note="similar to rat DNase I; chromatin-bound"
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/protein_id="AAC28937.1"
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BASE COUNT      351 a 333 c 320 g 327 t
ORIGIN

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Query Match		74.7%; Score 501.4; DB 10; Length 1331;
Best Local Similarity		85.3%; Pred. No. 1.1e-125;
Matches 559; Conservative		0; Mismatches 96; Indels 0; Gaps 0;
QY	1	ACAACAGGATCTGCCCATCTGATGAGAGAGTAAACGGAATTCAGAAAGGCATAA 60
Db	358	ACAACAACTCTGTCCTCATCTGATGAGAGAGTAAACGGAATTCAGAAAGGCATCA 417
QY	61	CATACAACTATGTGATTAGTCTCTCGCTTGGAAAGAACACATATAAGAACAGTATGCCT 120
Db	418	CATACAACTACGTGATTAGTCTCTCGCTTGGAAAGAACACATATAAGAACAGTATGCCT 477
QY	121	TTCTCTATAAGAAAGCTAGTCTGTGTAAACAAAGCTTACCTTACCGAGCTATCAGG 180
Db	478	TCCTCTACAGGAGAGCTGGTCTGTGTAAAGCAAAATACCTTACCATGACTATCAGG 537
QY	181	CTGGAGACCGAGATGTTTCCAGGAGACCTTTCTGGTCTGGTTCAGTACCCCTACA 240
Db	538	ATGGAGACAGACGCTGTTTCCAGGAGACCTTTCTGGTCTGGTTCAGGAGCCCTTCA 597
QY	241	CCGCTCTCAAGGACTTCGTGATTGTCCTCCCTGCACACACCTGAGACATCCGTTAGAG 300
Db	598	CTGCTCCCAAGGACTTCGTGATTGTCCTCCCTGCACACACCTGAGACATCCGTTAAG 657
QY	301	AGATTGATGAGCTGGTGTATCTACACAGATGTGAACCGTCCCTGGAATGCAGAGAAAT 360
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Db	718	TCATTTTTCATGGTGACTTCAATGCTGGCTGACGATAGCTCCCAAGAGGCTGGAAGG 777
QY	421	ACATCCGCTGAGGACGACCCCAAGTTCGTTGGCTGATCGGGGACCAAGGACACCA 480
Db	778	ACATCCGTTTGAGGACAGACCCCAAGTTCGTTGGCTGATCGGGGACCAAGGACACCA 837
QY	481	CGGTCAAGAGAGCAACAACTGCGCTTATGACAGGATCGTGTCTAGAGGACAAATATTG 540
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QY	601	CTGAATCGAAGGCTGGATGTGAGGACCACTTTCCAGTTCATCATCATCA 655
Db	958	CTGAAGAGGAGGCTGGATGTGAGGACCACTTTCCAGTTCATCATCATCA 1012
RESULT 10		
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LOCUS		Rattus norvegicus DNase gamma mRNA, complete cds.
DEFINITION		U75689
ACCESSION		U75689.1 GI:3220024
VERSION		
KEYWORDS		Rattus norvegicus.
SOURCE		Rattus norvegicus
ORGANISM		Rattus norvegicus
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS		Shiokawa,D., Ohyama,H., Yamada,T., Takahashi,K. and Tanuma,S.
TITLE		Identification of an endonuclease responsible for apoptosis in rat thymocytes
JOURNAL		Eur. J. Biochem. 226 (1), 23-30 (1994)
MEDLINE		95045594
PUBMED		7957253
REFERENCE		2 (bases 1 to 1417)
AUTHORS		Shiokawa,D. and Tanuma,S.
TITLE		Molecular cloning and expression of a cDNA encoding an apoptotic endonuclease DNase gamma
JOURNAL		Biochem. J. 332 (Pt 3), 713-720 (1998)
MEDLINE		98285539
PUBMED		9620874
REFERENCE		3 (bases 1 to 1417)
AUTHORS		Shiokawa,D. and Tanuma,S.
TITLE		Direct Submission
JOURNAL		Submitted (22-OCT-1996) Biochemistry, Science Univ. of Tokyo, Shinjuku-Ku Ichigaya funagawaracho, Tokyo 162, Japan
FEATURES		Location/Qualifiers
source		1..1417
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		203..1135
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		/product="DNase gamma"
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		/db_xref="GI:3220025"
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BASE COUNT		386 a 353 c 333 g 345 t
ORIGIN		
Query Match		74.7%; Score 501.4; DB 10; Length 1417;
Best Local Similarity		85.3%; Pred. No. 1.1e-125;
Matches 559; Conservative		0; Mismatches 96; Indels 0; Gaps 0;
QY	1	ACAACAGGATCTGCCCATCTGATGAGAGAGCTAAACGGAATTCAGAAAGGCATAA 60
Db	408	ACAACAACTCTGTCCCATCTGATGAGAGAGCTGAATGGAATTCACGAAAGCACGA 467
QY	61	CATACAACTATGTGATTAGTCTCTCGCTTGGAAAGAACACATATAAGAACAGTATGCCT 120
Db	468	CATACAACTATGTGATTAGTCTCTCGCTTGGAAAGAACACATATAAGAACAGTATGCCT 527
QY	121	TTCTCTATAAGAAAGCTAGTGTCTGTAAAAACAAAGCTTACCTTACCAAGCTATCAGG 180
Db	528	TCCTCTCAAGAGAGAGCTGGTGTCTGTGAAGGCAAAATACCTCTACCATGACTATCAGG 587
QY	181	CTGGAGACCGAGATGTGTTTCCAGGGAACCTTTGTGGTCTGGTTCAGTCAACCTACA 240
Db	588	ATGGAGACACAGACGCTGTTTCCAGGAGCCCTTTGTGGTTCAGAGGCGCCCTTCA 647
QY	241	CCGCTGTCAAGGACTTCGTGATTGTCCTCCCTGCACACACCTCTGAGACATCCGTTAGAG 300
Db	648	CTGCTGCCAAGGACTTCGTGATTGTCCTTGCACACAACCTCTGAAACCTCCGTTAAG 707
QY	301	AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAGAGCTCGCTGGAAATGCAGAGAAAT 360
Db	708	AGATAGATGAGCTGCTGACGCTCTACACGATGTGAGAAGACGATGGAAGGACAGAAAT 767
QY	361	TCATTTTTCATGGTGACTTCAATGCTGGCTGACGATAGCTGCTCCCAAGAGGCTGGAAGG 420
Db	768	TCATTTTTCATGGTGACTTCAATGCTGGCTGACGATAGCTGCTCCCAAGAGGCTGGAAGG 827
QY	421	ACATCCGCTGAGGACGACCCCAAGTTCGTTGGCTGATCGGGGACCAAGGACACCA 480
Db	828	ACATCCGTTTGAGGACAGACCCCAAGTTCGTTGGCTGATCGGGGACCAAGGACACCA 887
QY	481	CGGTCAAGAGAGCAACAACTGCGCTTATGACAGGATCGTGTCTAGAGGACAAATATTG 540
Db	888	CGGTCAAGAGAGCAACAGCTGTGCTTATGACAGGATGTGCTTCGGGACCAAGAGATAG 947
QY	541	TCAACTCTGGTCTCTCAATCAAACTCGTCTTGAATTCAGAAAGCTTACAGTTGT 600
Db	948	TCAACTCTGGTCTCTCAATCAAACTCGTCTTGAATTCAGAAAGCTTACAGTTGT 1007

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QY 601 CTGAATCGAAGGCGCTGATGTCACGACCACTTTCAGTTCATCATCATCAATCA 655
Db 1008 CTGAAGAGAGGCGCTGATGTCAGTGAACACTTTCAGTTCAGTTCAGTTCAGT 1062

RESULT 11
AR047845 1208 bp DNA linear PAT 29-SEP-1999
LOCUS AR047845
DEFINITION Sequence 2 from patent US 5821103.
ACCESSION AR047845
VERSION AR047845.1 GI:5970188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1208)
AUTHORS Tanuma,S.-i.
TITLE Deoxyribonuclease
JOURNAL Patent: US 5821103-A 2 13-OCT-1998;
FEATURES Location/Qualifiers
source 1..1208
BASE COUNT 319 a 304 c 283 g 302 t
ORIGIN
Query Match 71.7%; Score 481.2; DB 6; Length 1208;
Best Local Similarity 85.1%; Pred. No. 3.5e-120;
Matches 550; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

QY 1 ACAACAGATCTGCCCTACTGATGAGAACTAAACGAAATTCAGAAAGCATTA 60
Db 217 ACAACAGATCTGCCCTACTGATGAGAACTAAACGAAATTCAGAAAGCATTA 276
QY 61 CATACAACTATGATGATGATCTCGCTTGGAGAAACATATTAAGAAACAGTATGCT 120
Db 277 CATACAACTATGATGATGATCTCGCTTGGAGAAACATATTAAGAAACAGTATGCT 336
QY 121 TTCTCTATTAAGAAAGCTAGTCTGTGTAACAAAGCTACCTTACGACGATATCAG 180
Db 337 TCCTCTAACAAGAGAGCTGCTGTGTAAGGCAAAATACCTTACCATGATCATCAGG 396
QY 181 CTGAGAGCGAGATGATGTTTTCAGAGGAACCTTGTGCTGCTTCCAGTCAACCTTACA 240
Db 397 ATGAGAGACAGAGCTGTTTTCAGAGGAGCCCTTGTGCTGCTTCCAGGAGCCCTTCA 456
QY 241 CCGCTGCAAGAGACTCTGATATTGCCCCCTGCAACACCCCTGAGACATCCGTTAGAG 300
Db 457 CTGCTGCCAAGAGACTCTGATATTGCCCCCTGCAACACCCCTGAGACATCCGTTAAG 516
QY 301 AGATTGATGAGCTGCTGATGTTACACAGATGTGAAACGTGCTGGAATGACAGAAAT 360
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QY 517 TCATTTTCATGAGTACTTCAATGCTGCTGAGTACGTCCTCCCAAGAGGCTTGAAG 420
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QY 421 ACATCCGCTGAGAGCGAGACCCCAAGTTCGTTTGGCTGATCGGGAGACCAAGAGACCA 480
Db 637 ACATCCGCTGAGAGCGAGACCCCAAGTTCGTTTGGCTGATCGGGAGACCAAGAGACCA 696
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QY 601 CTGAATCGAAGGCGCTG---GATGTCAGAGCACTTTCAGTTCA 643
Db 817 CTGAAGAGAGGCGCTGATGTCAGTGAACCACTTTCAGTTCA 862
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RESULT 12
E11687 1208 bp RNA linear PAT 29-SEP-1997
LOCUS E11687
DEFINITION cDNA encoding novel deoxyribonuclease (DNase) gamma which cut
specifically linker site of chromatin DNA.
ACCESSION E11687
VERSION E11687.1 GI:22025323
KEYWORDS JP 1996187079-A/1.
SOURCE Rattus rattus.
ORGANISM Rattus rattus.
REFERENCE 1 (bases 1 to 1208)
AUTHORS Tanuma,Y.
TITLE NEW DEOXYRIBONUCLEASE
JOURNAL Patent: JP 1996187079-A 1 23-JUL-1996;
TANUMA YASUKAZU
OS Rattus rattus (rat)
PN JP 1996187079-A/1
PD 23-JUL-1996
PF 06-SEP-1995 JP 1995255647
PR 06-SEP-1994 JP 94P 239518
PI TANUMA YASUKAZU
PC C12N9/16,C07K14/47,C07K16/40,C12N1/21,C12N15/09,(C12N1/21,PC
C12N1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT source 1..1208
FT FT /organism='Rattus rattus'
FT FT /tissue_type='Thymus, Spleen' FT
FT CDS 1..11
FT FT /product='Novel deoxyribonuclease (DNase) gamma
FT FT which cut
FT FT specifically linker site of chromatin DNA' FT
FT Precursor RNA 12..86
FT FT Location/Qualifiers
FEATURES
source 1..1208
BASE COUNT 319 a 304 c 283 g 302 t
ORIGIN
Query Match 71.7%; Score 481.2; DB 6; Length 1208;
Best Local Similarity 85.1%; Pred. No. 3.5e-120;
Matches 550; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

QY 1 ACAACAGATCTGCCCTACTGATGAGAACTAAACGAAATTCAGAAAGCATTA 60
Db 217 ACAACAGATCTGCCCTACTGATGAGAACTAAACGAAATTCAGAAAGCATTA 276
QY 61 CATACAACTATGATGATGATCTCGCTTGGAGAAACATATTAAGAAACAGTATGCT 120
Db 277 CATACAACTATGATGATGATCTCGCTTGGAGAAACATATTAAGAAACAGTATGCT 336
QY 121 TTCTCTATTAAGAAAGCTAGTCTGTGTAACAAAGCTACCTTACGACGATATCAG 180
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QY 181 CTGAGAGCGAGATGATGTTTTCAGAGGAACCTTGTGCTGCTTCCAGTCAACCTTACA 240
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Qy 421 ACATCCGCTGAGGACGACCCCAAGTTCGTTGGCTGATCGGGGACCAAGAGACACCA 480
Db 637 ACATCCGTTGAGGACAGACCCCAACTTTGTTGGCTGATGAGGACCAAGAGACACCA 696
Qy 481 CGTCAAGAGAGACCAAACTGCGCTATGACAGGATCGTCTTAGAGGACAAATATTG 540
Db 697 CGTCAAGAGAGACCAAGCTGTGCTATGACAGGATGTGCTGCGGACAGAGATAG 756
Qy 541 TCAACTCTGCTGCTCTCAATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGTTGT 600
Db 757 TCAACTCTGCTGTTCCCGCTCCAGTGGCTCTTTGACTTTCAAGAAAGCTTATGAGTTGT 816
Qy 601 CTGAATCGAAGGCCCTG--GATGTCAGCAGCACCTTCCAGTTCA 643
Db 817 CTGAAGAGAGGCCCTGGATGATGTGAGTACCACTTTCAGTTGA 862

RESULT 13
MMU76110
LOCUS Mus musculus DNase gamma mRNA, complete cds.
DEFINITION
ACCESSION U76110
VERSION U76110.1 GI:4098207
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Shikawa, D., Hatanaka, T. and Tanuma, S.
JOURNAL Direct Submission
Submitted (24-Oct-1996) Biochemistry, Science Univ. of Tokyo,
Shinjuku-ku ichigaya funagawaracho, Tokyo 162, Japan
FEATURES
Location/Qualifiers
1..941
/organism="Mus musculus"
/strain="C57 black"
/db_xref="taxon:10090"
7..939
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/feature="deoxyribonuclease"
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TPTSTVEIDELVDYIDVRSQWKTEPFIFMGDFNAGCSYVPRKAWQNRIRLTPKF
VWLIGQEDTIVKSTCAYDRIVLCQEIIVNSVVRSSGVDFQKAYDLSEEDALDY
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BASE COUNT 255 a 229 c 228 g 229 t
ORIGIN

Query Match 70.8%; Score 474.8; DB 10; Length 941;
Best Local Similarity 82.9%; Pred. No. 1.9e-118;
Matches 542; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Qy 2 CAACAGATCTGCCCATCTGATGAGAGCTTAACGGAAATTCAGAAAGGCATAC 61
Db 213 CAACAAATCTGTCCCATCTGATGAGAGCTGAATGAAATTCAGAAAGGCACAC 272
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Qy 62 ATACAACATATGATTAGCTCTGCGCTTGGAAGAAACACATATAAAGACAGTATGCCCTT 121
Db 273 ATACAACATATGATTAGTTCGACTTTGGAAGAAACACATATAAAGACAGTATGCCCTT 332
Qy 122 TCTCTATAAAGAAAGCTAGTGTCTGTAACAAAGCTACCTCTACACAGCTATCAGGC 181
Db 333 CGTCTACAAGGAGAGCTGTGTCTGTGAAGACAAATACCACTACATGACTATCAGGA 392
Qy 182 TGAGACGCGAGATGTGTTTTCCAGGGAACCTTTGTGCTCCAGTTCACCCCTACAC 241
Db 393 TGAGACACAGACGTTGTTTTCCAGGAGGCCCTTTGTGTTTGGTTCCATTCCTTTTAC 452
Qy 242 CGTGTCAAGGACTTCGTGATTTGCCCTTGACACACCCCTGACAGATCGCTTAGAGA 301
Db 453 TGTGTCAAGGACTTCGTGATTTGCCCTTGACACAACTCCCGAGACCTCCGTTAAAGA 512
Qy 302 GATTGATGAGCTGGCTGATGTCTACACAGATGTGAACCGCTCGCTGGAATGCAGAGAAAT 361
Db 513 GATGATGAGCTGGCTGATGTCTACCGATGTGGAAGCCAGTGGAGACAGAGAAATTT 572
Qy 362 CATTTTCATGSGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAGGCCTTGAAGGA 421
Db 573 CATCTTCATGSGGTGATTTCAACGCGCTGTAGCTATGTCCCCAAGAGGCCTTGGCAGAA 632
Qy 422 CATCCGCTGAGGACGAGACCCCAAGTTTCTGTTGGCTGATCGGGGACCAAGAGACACAC 481
Db 633 CATTCGTTTGAAGACGAGACCCCAAGTTTCTGTTGGCTGATGTTGGGACCAAGAGGACACTAC 692
Qy 482 GGTCAAGAGAGACCAAACTGCGCTATGACAGGATCGCTTAGAGGACAAATATTGT 541
Db 693 GGTCAAGAGAGATACAGCTGTGCTTATGACAGGATGTGCTTTGTTGGACAGAGATAGT 752
Qy 542 CAACTCTGCTGCTCTCAATCAAACTCTCTTTGATTTCCAGAAAGCTTACAGGTTGTC 601
Db 753 CAACTCCGTTGTTCCCGCTTCCAGTGGCTCTTTGACTTTTCAGAAAGCTTATGACTTGT 812
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Db 813 TGAGGAGGAGGCCCTGGATGTCAGTGCATGATCAGTTTCCAGTTGAGTTTAAAGCTACA 866

RESULT 14
AF047355
LOCUS Mus musculus liver and spleen DNase precursor (LSD) mRNA, complete
DEFINITION cds.
ACCESSION AF047355
VERSION AF047355.1 GI:2905787
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 1124)
Cloning and characterization of an actin-resistant DNase I-like
endonuclease secreted by macrophages
JOURNAL Gene 215 (2), 291-301 (1998)
MEDLINE 98382522
PUBMED 9714828
REFERENCE 2 (bases 1 to 1124)
AUTHORS Baron, W.F., Pan, C.Q., Spencer, S.A., Ryan, A.M., Lazarus, R.A. and
Baker, K.P.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1998) Molecular Biology, Genentech Inc., 1 DNA
Way, South San Francisco, CA 94080, USA
FEATURES
Location/Qualifiers
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I; LS-DNase"
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/ translation="MSLHPASPRLASLILFLALHDTLALRLCSFNVRSFGASKENH
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173..247
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/ gene="LSD"
/ product="liver and spleen DNase"
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Query Match      70.8%; Score 474.8; DB 10; Length 1124;
Best Local Similarity 82.9%; Pred. No. 1.9e-118;
Matches 542; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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379 CAACACATCTGTCCCATCTGATGAGAGCTGAATGGAATTCACGAAAGACACAA 438
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62 ATACACATAGTATGATCTGCTCGCCCTTGGAAGAAACATATAAGAACATAGCCTT 121
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439 ATACACATAGTATGATCTGCTCGCCCTTGGAAGAAACATATAAGAACATAGCCTT 498
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499 CGTCAACAAGAGAGAGCTGTCTGTGAAGACAAATAACACATACATGATATCAGGA 558
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182 TGGAGACCAAGATGTGTTTTCCAGGAAACCTTTGTGTCTGTGTTCCAGTACCTTAAC 241
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559 TGGAGACCAAGATGTGTTTTCCAGGAAACCTTTGTGTGTTCCATTCCTCCCTTAC 618
|||||
242 CGCTGTCAAGAGCTGTGATGTTGCTCCCTGACACACCCCTGAGACATCCGTAGAGA 301
|||||
619 TGCTGTCAAGAGCTGTGATGTTGCTCCCTGACACACACCTCCGAGACCTCCGTAAAGA 678
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302 GATTGATAGCTGTGATGTTGTTACACAGATGTGAAACGTGCTGGAATGACAGAAATTT 361
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679 GATGATAGCTGTGATGTTGTTACACAGATGTGAAACGTGGAAGACAGAAATTT 738
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739 CATCTTCATGGTGATTTCAACGCGGCTGTAGCTATGTTCCCAAGAAAGGCTGTGCAAA 798
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422 CATCGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 481
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799 CATTCGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858
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482 GGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541
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859 GGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
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542 CAATCTGTGTGTCTCTCAATCAAACTGTCTTTGATTTCCAGAAAGCTTACAGTTGTC 601
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919 CAATCTGTGTGTCTCTCAATCAAACTGTCTTTGATTTCCAGAAAGCTTACAGTTGTC 978
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602 TGAATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 655
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BC012671
LOCUS      BC012671      2110 bp      mRNA      linear      ROD 07-AUG-2002
DEFINITION Mus musculus, similar to deoxyribonuclease 1-like 3, clone
MGC:13854 IMAGE:4160709, mRNA, complete cds.
ACCESSION BC012671
VERSION   BC012671.1
KEYWORDS  GI:15215118
SOURCE    house mouse.
ORGANISM Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2110)
AUTHORS   Strausberg, R.
TITLE      Direct Submission
JOURNAL    Submitted (15-AUG-2001) National Institutes of Health, Mammalian
           Gene Collection (MGC), Cancer Genomics Office, National Cancer
           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
           USA
REMARK     NIH-MGC Project URL: http://mgc.ncl.nih.gov
           Contact: MGC help desk
           Email: cgabs-rc@mail.nih.gov
           Tissue Procurement: Jeffrey E. Green, M.D.
           CDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: Institute for Systems Biology
           http://www.systemsbio.org
           contact: amadan@systemsbiology.org
           Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
           Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIN at: http://image.llnl.gov
Series: IRAK Plate: 18 Row: 1 Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6681204.
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/tissue_type="Liver, normal. 5 month old male mouse."
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BASE COUNT      526 a      581 c      464 g      539 t
ORIGIN
Query Match      70.5%; Score 473.2; DB 10; Length 2110;
Best Local Similarity 82.7%; Pred. No. 5.5e-118;
Matches 541; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

2 CAACAGATCTGCCCATCTAGTGAAGAGCTAAACGGAATTCAGAAAAGCATAC 61
|||||
357 CAACACATCTGTCCCATCTGATGAGAGAGCTGAATGGAATTCAGAAAGACACAAT 416
|||||
62 ATACACATAGTATGATCTGCTCGCCCTTGGAAGAAACATATAAGAACATAGTGCCTT 121
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417 ATACACATAGTATGATCTGCTCGCCCTTGGAAGAAACATATAAGAACATAGTGCCTT 476
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122 TCTCTATAAGAAAAGCTAGTGTCTGTAACAAAGCTACCTCTACAGAGCTATCAGGC 181
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Db 477 CGTCTACAAGGAGAACTGGTGTCTGTGAAGACAAATACCACTACCATGACTATCAGGA 536
Qy 182 TGGAGACGAGATGTGTTTCCAGGAACCTTTGTGGTCTGGTCCAGTCCACCTACAC 241
Db 537 TGGAGACACAGACGCTGTTTCCAGGAGCCCTTTGTGGTTGGTTCCATTCCCCCTTAC 596
Qy 242 CGCTGTCAAGGACTTCGTGATGTGTCCTCCCTGCACACCCCTGAGACATCCGTTAGAA 301
Db 597 TCGTGTCAAGGACTTCGTGATGTGTCCTCCCTTGACACAACCTCCGAGACCTCCGTTAAGA 656
Qy 302 GATTGATGAGCTGGCTGATGTCTACACAGATGTGAACGTCGCTGGAATGCAGAGAATTT 361
Db 657 GATAGATGAGCTGGTCTGATGTCTACACGATGTGAAGCCAGTGAAGACAGAGAATTT 716
Qy 362 CATTTTCATGGGTGACTTCAATGCTGGCTGCAGCTACGTCCCCAAGAAGCCCTGGAAGGA 421
Db 717 CATCTTCATGGGTGATTTCAACGCGGCTGTAGCTATGTCCCCAAGAAGCCCTGGCAGAA 776
Qy 422 CATCCGCTGAGGACGGACCCCAAGTTGTTGGCTGATCGGGGACCAAGAGACACAC 481
Db 777 CATTCGTTTGAGGACGGACCCCAAGTTGTTGGCTGATGGGGACCAAGAGGACACTAC 836
Qy 482 GGTCAAGAAAGACACAAACTGCGCCTATGACAGGATCGTGTAGAGGACAAATATTCT 541
Db 837 GGTCAAGAAAGATACAGCTGTGCTTATGACAGGATGTGCTTTGGGACAAAGATAGT 896
Qy 542 CAACTCTGGTGTCTCTCAATCAAACTCGTCTTTGATTTCCAGAAAAGCTTACAGGTTGTC 601
Db 897 CAACTCCGTGGTTCCCGGTTCCAGTGGCGTCTTTGACTTTCAAGAAAGCTTATGACTTGC 956
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Db 957 TGAGGAGGAGGCCCTGGATGTGAGTGCATCATCTTCCAGTTGAGTTTAAGCTACA 1010

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Job time : 1421.41 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2002, 08:59:14 ; Search time 193.384 Seconds
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Title: US-09-905-114-3

Perfect score: 671

Sequence: 1 aacacagatctgcccata.....atcatcatgaagaaccatga 671

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	527	78.5	1023	24	ABL61914
6	527	78.5	1023	24	ABL64458
7	527	78.5	1023	24	ABL64961
8	527	78.5	1079	18	AAT74076
9	525.4	78.3	1108	24	ABK84429

10	518.4	77.3	556	24	AAS17901	Partial cDNA encod
11	479.6	71.5	1208	17	AAT17733	Deoxyribonuclease,
12	474.8	70.8	1124	18	AAT74083	Murine LS-DNase nu
13	348.4	51.9	350	24	AAS17902	partial cDNA encod
14	314.8	46.9	350	24	AAS17903	partial cDNA encod
15	300.6	44.8	349	24	AAS17904	Partial cDNA encod
16	195.6	29.2	392	24	ABN94132	Gene #630 used to
17	195.6	29.2	392	24	ABL62246	Human DNase I. HO
18	163.2	24.3	1039	15	AAQ54429	Colon adenocarcino
19	163.2	24.3	1039	22	ABA02661	Human DNase I. HO
20	161.6	24.1	783	22	ABA02662	Human DNase I. HO
21	161.6	24.1	858	22	ABA02663	Human DNase I. HO
22	161.6	24.1	1000	21	AAA28433	DNA encoding stii
23	161.6	24.1	1039	11	AAQ05512	Sequence encoding
24	161.6	24.1	1039	15	AAQ05512	Human DNase gene.
25	161.6	24.1	1548	22	ABA02702	Humanised HMFG-1 F
26	161.6	24.1	1548	22	ABA02703	Humanised HMFG-1 F
27	161.6	24.1	1548	22	ABA02705	Humanised HMFG-1 F
28	161.6	24.1	1554	22	ABA02682	Humanised HMFG-1 F
29	161.6	24.1	1554	22	ABA02683	Humanised HMFG-1 F
30	161.6	24.1	1554	22	ABA02685	Humanised HMFG-1 F
31	161.6	24.1	1557	22	ABA02704	Humanised HMFG-1 F
32	161.6	24.1	1560	22	ABA02710	Humanised HMFG-1 F
33	161.6	24.1	1560	22	ABA02711	Humanised HMFG-1 F
34	161.6	24.1	1560	22	ABA02713	Humanised HMFG-1 F
35	161.6	24.1	1560	22	ABA02714	Humanised HMFG-1 F
36	161.6	24.1	1560	22	ABA02715	Humanised HMFG-1 F
37	161.6	24.1	1560	22	ABA02716	Humanised HMFG-1 F
38	161.6	24.1	1563	22	ABA02684	Humanised HMFG-1 F
39	161.6	24.1	1566	22	ABA02706	Humanised HMFG-1 F
40	161.6	24.1	1566	22	ABA02707	Humanised HMFG-1 F
41	161.6	24.1	1566	22	ABA02709	Humanised HMFG-1 F
42	161.6	24.1	1569	22	ABA02712	Humanised HMFG-1 F
43	161.6	24.1	1575	22	ABA02708	Humanised HMFG-1 F
44	161.6	24.1	1578	22	ABA02717	Humanised HMFG-1 F
45	161.6	24.1	1578	22	ABA02718	Humanised HMFG-1 F

ALIGNMENTS

RESULT 1
AAD29089
ID AAD29089 standard; DNA; 671 BP.
XX
AC AAD29089;
XX
DT 16-MAY-2002 (first entry)
XX
DE Bovine 22kDa recombinant FAA (rFAA) coding sequence.
XX
DE Bovine; fertility associated antigen; FAA; sperm fertility; acrosome;
KW artificial insemination; plasma membrane; sperm cell; anti-infertility;
KW reproductive tract; ds.
XX
OS Bos sp.
XX
PN WO200206444-A2.
XX
PD 24-JAN-2002.
XX
PF 16-JUL-2001; 2001WO-US22097.
XX
PR 14-JUL-2000; 2000US-218140P.
XX
PA (ARIZ-) ARIZONA BOARD OF REGENTS.
XX
PI Zhang H, Ax RL, Bellin ME;
XX
DR WPI; 2002-171803/22.
XX
PT Novel amino acid and polynucleotide sequence for fertility associated antigen useful for increasing stability of plasma membrane, acrosome

PT and other portions of sperm cell, and increasing fertility of mammals
 XX
 PS Claim 1; Fig 5; 37pp; English.
 XX

CC The invention relates to bovine fertility associated antigen (FAA) and
 CC its nucleic acid sequence. FAA is useful for increasing the stability of
 CC the plasma membrane plus acrosome of a sperm cell and/or other portions
 CC of a sperm cell, in particular mammalian sperm cell such as a sperm cell
 CC from buffalo, cow, horse, mice, pig, sheep, human, avian sperm cell
 CC including turkey or chicken sperm cell. FAA is also useful for increasing
 CC the fertility of sperm from a mammal including buffalo, cow, horse, mice,
 CC pig, sheep or human, or avian (chicken or turkey). FAA is added to the
 CC suspension of sperm cells prior to preservation or prior to
 CC administration of the sperm cells to a mammal in artificial insemination.
 CC Alternatively, fertility of sperm from a mammal is increased by placing
 CC FAA into a female's reproductive tract prior to deposition of the sperm
 CC cells into the female's reproductive tract by copulation or artificial
 CC insemination. The fertility of the male mammal is increased by injecting
 CC FAA into the male mammal's reproductive tract. The present sequence is
 CC bovine 22kDa recombinant FAA (rFAA) coding sequence.
 CC
 SO Sequence 671 BP; 195 A; 166 C; 154 G; 156 T; 0 other;

Query Match 100.0%; Score 671; DB 24; Length 671;
 Best Local Similarity 100.0%; Pred. No. 4e-202;
 Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAACAGAGTCTGCCCTACTGATGAGAGCTTAACGGAATTCAGAAAAAGCATATA 60
 DB 1 ACAACAGATCTGCCCTACTGATGAGAGCTTAACGGAATTCAGAAAAAGCATATA 60
 QY 61 CATACACTATGTGATGATGCTCTGCTTGAAGAAACATATTAAGAAGCATATGCTCT 120
 DB 61 CATACACTATGTGATGATGCTCTGCTTGAAGAAACATATTAAGAAGCATATGCTCT 120
 QY 121 TTCTTATAAAGAAAGCTAGTGTGTTAAAAAGCTACTCTCAACCACTTATCAGG 180
 DB 121 TTCTTATAAAGAAAGCTAGTGTGTTAAAAAGCTACTCTCAACCACTTATCAGG 180
 QY 181 CTGAGACGAGATGTGTTTCCAGGAAACCTTGTGTGTTGTTCCAGTACCCCTACA 240
 DB 181 CTGAGACGAGATGTGTTTCCAGGAAACCTTGTGTGTTGTTCCAGTACCCCTACA 240
 QY 241 CCGCTGTCAAGACTTGTGATGTGCTCCCTGACACCAACCCCTGAGACATCCGTTAAG 300
 DB 241 CCGCTGTCAAGACTTGTGATGTGCTCCCTGACACCAACCCCTGAGACATCCGTTAAG 300
 QY 301 AGATTGAGACTGGCTGATGCTACAGATGTAACGTCGCTGGAATGAGAGATT 360
 DB 301 AGATTGAGACTGGCTGATGCTACAGATGTAACGTCGCTGGAATGAGAGATT 360
 QY 361 TCATTTTATGAGTACTTCAATGCTGAGCTAGTCCCAAGAGAGCTTGAAGG 420
 DB 361 TCATTTTATGAGTACTTCAATGCTGAGCTAGTCCCAAGAGAGCTTGAAGG 420
 QY 421 ACATTCGCTTGAAGACGAGACCCCAAGTTCGTTGCTGATGCGGGAGCAAGAGACCA 480
 DB 421 ACATTCGCTTGAAGACGAGACCCCAAGTTCGTTGCTGATGCGGGAGCAAGAGACCA 480
 QY 481 CGGTCAAAAGAGCAAACTGCGCTTATGACAGATGCTGTTAGAGACAAAATATTG 540
 DB 481 CGGTCAAAAGAGCAAACTGCGCTTATGACAGATGCTGTTAGAGACAAAATATTG 540
 QY 541 TCAACTCTGAGTCTCAATCAAACTGCTTGTGATTTCCAGAAAGCTTACAGATTGT 600
 DB 541 TCAACTCTGAGTCTCAATCAAACTGCTTGTGATTTCCAGAAAGCTTACAGATTGT 600
 QY 601 CTGAATCGAAGGCCCTGATGTCAAGCACTTTCCAGTTTCATCATCATCATCATCATG 660
 DB 601 CTGAATCGAAGGCCCTGATGTCAAGCACTTTCCAGTTTCATCATCATCATCATCATG 660
 QY 661 AAGAACCATGA 671

DB 661 AAGAACCATGA 671

RESULT 2

ID AAD29088 standard; cDNA; 592 BP.

AC AAD29088;

DT 16-MAY-2002 (first entry)

DE Bovine fertility associated antigen (FAA) partial cDNA.

XX Bovine; fertility associated antigen; FAA; sperm fertility; acrosome;

KW artificial insemination; plasma membrane; sperm cell; anti-fertility;

XX reproductive tract; ss.

OS Bos sp.

XX Key

FT Location/Qualifiers

FT 1..591

FT CDS

PF 16-JUL-2001; 2001WO-US22097.

PR 14-JUL-2000; 2000US-218140P.

PA (ARIZ-) ARIZONA BOARD OF REGENTS.

XX Zhang H, Ax RL, Bellin ME;

DR WPI; 2002-171803/22.

DR P-PSDB; AAE18281.

PT Novel amino acid and polynucleotide sequence for fertility associated

PT antigen useful for increasing stability of plasma membrane, acrosome

PT and other portions of sperm cell, and increasing fertility of mammals

PS Claim 1; Fig 6; 37pp; English.

CC The invention relates to bovine fertility associated antigen (FAA) and

CC its nucleic acid sequence. FAA is useful for increasing the stability of

CC the plasma membrane plus acrosome of a sperm cell and/or other portions

CC of a sperm cell, in particular mammalian sperm cell such as a sperm cell

CC from buffalo, cow, horse, mice, pig, sheep, human, avian sperm cell

CC including turkey or chicken sperm cell. FAA is also useful for increasing

CC the fertility of sperm from a mammal including buffalo, cow, horse, mice,

CC pig, sheep or human, or avian (chicken or turkey). FAA is added to the

CC suspension of sperm cells prior to preservation or prior to

CC administration of the sperm cells to a mammal in artificial insemination.

CC Alternatively, fertility of sperm from a mammal is increased by placing

CC FAA into a female's reproductive tract prior to deposition of the sperm

CC cells into the female's reproductive tract by copulation or artificial

CC insemination. The fertility of the male mammal is increased by injecting

CC FAA into the male mammal's reproductive tract. The present sequence is

CC bovine fertility associated antigen (FAA) partial cDNA.

SO Sequence 592 BP; 170 A; 143 C; 142 G; 137 T; 0 other;

Query Match 88.2%; Score 592; DB 24; Length 592;

Best Local Similarity 100.0%; Pred. No. 4.1e-177;

Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GAGAGCTAAAGGAAATTCAGAAAAAGCATATCACTATGATGATGCTCTGCGC 86

Db	1	GAGAAGCTAAACCGAAATTCAGAAAGGATACATACAACTATGTGATTAGCTCTCGC	60
QY	87	CTTGGGAAGAAACACATATAAAGACAGTATGCTTCTCTATAAAGAAAAGCTAGTGCT	146
Db	61	CTTGGGAAGAAACACATATAAAGACAGTATGCTTCTCTATAAAGAAAAGCTAGTGCT	120
QY	147	GTAAAAAAGCTACCTCTTACACGACTATCAGGCTGGAGACGAGATGTTTCCAGG	206
Db	121	GTAAAAAAGCTACCTCTTACACGACTATCAGGCTGGAGACGAGATGTTTCCAGG	180
QY	207	GAACCTTTTGTGCTCTGCTTCCAGTACCCCTACACGCTGTCAAGGACTTCGTGATGTC	266
Db	181	GAACCTTTTGTGCTCTGCTTCCAGTACCCCTACACGCTGTCAAGGACTTCGTGATGTC	240
QY	267	CCCTGTCACACACCCCTGAGACATCGTTAGAGAGATTGATGAGCTGGCTGATGCTAC	326
Db	241	CCCTGTCACACACCCCTGAGACATCGTTAGAGAGATTGATGAGCTGGCTGATGCTAC	300
QY	327	ACAGATGTGAACGCTCGCTGGAATGCAGAGAATTTCAATTTTCATGGGTGACTTCAATGCT	386
Db	301	ACAGATGTGAACGCTCGCTGGAATGCAGAGAATTTCAATTTTCATGGGTGACTTCAATGCT	360
QY	387	GGCTGAGTACCTCCCAAGAGGCTGGAAGGACATCCGCTGAGGACGACCCCAAG	446
Db	361	GGCTGAGTACCTCCCAAGAGGCTGGAAGGACATCCGCTGAGGACGACCCCAAG	420
QY	447	TTGCTTTGGCTGATCGGGACCAAGAGGACACCCGCTCAAGAGAGCAAACTCGGC	506
Db	421	TTGCTTTGGCTGATCGGGACCAAGAGGACACCCGCTCAAGAGAGCAAACTCGGC	480
QY	507	TATGACAGGATCGTGTAGAGGACAAAATATTTGTCAACTCTGCTGCTCAATCAAAAC	566
Db	481	TATGACAGGATCGTGTAGAGGACAAAATATTTGTCAACTCTGCTGCTCAATCAAAAC	540
QY	567	CTGCTCTTTGATTTCCAGAAAGCTTACAGTTGCTGTAATCGAAGGCCCTGG	618
Db	541	CTGCTCTTTGATTTCCAGAAAGCTTACAGTTGCTGTAATCGAAGGCCCTGG	592
RESULT 3			
AA517900			
ID	AA517900	standard; cDNA; 578 BP.	
XX	AA517900;		
AC	AA517900;		
XX	26-MAR-2002	(first entry)	
DT			
XX	DNA encoding bovine fertility-associated antigen (FAA).		
DE			
XX	Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome;		
KW	reproductive fitness; single nucleotide polymorphism; SNP; bovine; cow;		
KW	ss.		
XX			
OS	Bos taurus.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	1..578	
FT		/tag= a	
FT		/product= "FAA"	
FT		/note= "Fertility-associated antigen"	
FT		/partial	
FT		/note= "No start or stop codon given"	
FT		/transl_except= (pos:289..300, aa:A)	
FT		/note= This codon has an apparent 9 nucleotide insertion	
FT		/transl_except= (pos:325..326, aa:R)	
FT		/note= "This codon has an apparent 1 nucleotide deletion which alters the reading frame"	
FT		/transl_except= (pos:576..578, aa:RLSRSKAL)	
XX			
PN	W0200176529-A2.		
XX			

PD	18-OCT-2001.		
XX			
PF	09-APR-2001; 2001WO-US10802.		
XX			
PR	07-APR-2000; 2000US-195225P.		
XX			
PA	(ZHAN/) ZHANG H M.		
PA	(AXRL/) AX R L.		
XX			
PI	Zhang HM, Ax RL;		
XX			
DR	WPI; 2002-066307/09.		
DR	P-PSDB; AAU11516.		
XX			
PT	Novel human or bovine fertility-associated antigen useful for		
PT	stabilising sperm cell acrosome and increasing fertility of a male		
PS	Claim 25; Fig 2A-E; 54pp; English.		
XX			
CC	The invention describes a novel isolated human fertility-associated		
CC	antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful		
CC	for increasing the stability of a sperm cell acrosome and for increasing		
CC	the fertility of a human male by administering FAA. Detecting single		
CC	nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful		
CC	for assaying fertility by detecting the presence or absence of a FAA SNP		
CC	in the mammal and correlating the presence or absence with the fertility		
CC	of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the		
CC	specification. FAA SNP is also useful for determining the reproductive		
CC	fitness of a human or bovine, by determining the nucleotide sequence of		
CC	the FAA SNP, quantifying the fertility of more than one mammal containing		
CC	the FAA SNP and correlating the frequency of the FAA SNP to the		
CC	reproductive fitness of the mammals. FAA improves the integrity of sperm		
CC	membranes and increases the capacitation of sperm derived from either		
CC	fertile or infertile humans. Early genetic identification of infertility		
CC	improves the prognosis for subsequent attempts at fertilisation and		
CC	facilitates early intervention to determine whether the individual may		
CC	benefit from fertility treatments to avoid costly and/or emotional		
CC	problems with attempted inseminations. This sequence encodes the bovine		
CC	fertility-associated antigen (FAA) described in the method of the		
XX	invention.		
XX			
SQ	Sequence 578 BP; 167 A; 140 C; 138 G; 133 T; 0 other;		
	Query Match 80.3%; Score 539; DB 24; Length 578;		
	Best Local Similarity 98.3%; Pred. No. 2.6e-160;		
	Matches 569; Conservative 0; Mismatches 0; Indels 10; Gaps 2;		
QY	27	GAGAAGCTAAACCGAAATTCAGAAAGGACATACAACTATGTGATTAGCTCTCGC	86
Db	1	GAGAAGCTAAACCGAAATTCAGAAAGGACATACAACTATGTGATTAGCTCTCGC	60
QY	87	CTTGGGAAGAAACACATATAAAGACAGTATGCTTCTCTATAAAGAAAAGCTAGTGCT	146
Db	61	CTTGGGAAGAAACACATATAAAGACAGTATGCTTCTCTATAAAGAAAAGCTAGTGCT	120
QY	147	GTAAAAAAGCTACCTCTTACACGACTATCAGGCTGGAGACGAGATGTTTCCAGG	206
Db	121	GTAAAAAAGCTACCTCTTACACGACTATCAGGCTGGAGACGAGATGTTTCCAGG	180
QY	207	GAACCTTTTGTGCTCTGCTTCCAGTACCCCTACACGCTGTCAAGGACTTCGTGATGTC	266
Db	181	GAACCTTTTGTGCTCTGCTTCCAGTACCCCTACACGCTGTCAAGGACTTCGTGATGTC	240
QY	267	CCCTGTCACACACCCCTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGAGTGGCT	317
Db	241	CCCTGTCACACACCCCTGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGAGTGGCT	300
QY	318	GATGCTCTACACAGATGTGAAAGCTCGCTGGAATGCAGAGAAATTTCAATTTTCATGGGTGAC	377
Db	301	GATGCTCTACACAGATGTGAAAGCTC-CTGGAATGCAGAGAAATTTCAATTTTCATGGGTGAC	359
QY	378	TTCAATGCTGCTGAGCTACGCTCCCAAGAGGCGCTGGAAGGACATCCGCTTGAGGACG	437

Db 360 TTCATGCTGCGTGCAGCTACGTCCTCCCAAGAGGCGCTGAGAGACATCCGCTGAGAGG 419
Oy 438 GACCCCAAGTTGTTGGCTGATCGGGGACCAAGAGACACCGTCAAGAAAGACACA 497
Db 420 GACCCCAAGTTGTTGGCTGATCGGGGACCAAGAGACACCGTCAAGAAAGACACA 479
Oy 498 AACTGCGCTATGACAGATCGTGCTTAAGAGCAAAATATTGTCAACTCTGCTGCTCT 557
Db 480 AACTGCGCTATGACAGATCGTGCTTAAGAGCAAAATATTGTCAACTCTGCTGCTCT 539
Oy 558 CAATCAAACTGCTGCTTTGATTTCCAGAAAGCTTACAG 596
Db 540 CAATCAAACTGCTGCTTTGATTTCCAGAAAGCTTACAG 578

RESULT 4
ABN96895
ID ABN96895 standard; DNA; 1023 BP.
XX
AC ABN96895;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #3393 used to diagnose liver cancer.
XX
KM Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KM metastatic liver tumour; cytostatic; expression profile; disease state;
KM disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30589.
XX
PR 02-OCT-2000; 2000US-237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX WPI; 2002-426119/45.
XX
PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample
XX
PS Claim 1; SEQ ID NO 3393; 298bp; English.
XX
XX The invention relates to a novel method for diagnosing and detecting the
XX progression of liver cancer, hepatocellular carcinoma or metastatic liver
XX tumour in a patient, and differentiating metastatic liver cancer from
XX hepatocellular carcinoma in a patient, involving detecting the level of
XX expression of two or more genes represented in ABN93503-ABN97455 in a
XX tissue sample. The method of the invention has hepatotropic, and
XX cytostatic activity. The method is useful for diagnosing and detecting
XX the progression of liver cancer, hepatocellular carcinoma and metastatic
XX liver carcinoma in a patient. The method is useful for identifying
XX expression profiles which serve as useful diagnostic markers as well as
XX markers that can be used to monitor disease states, disease progression,
XX drug toxicity, drug efficacy and drug metabolism.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1023 BP; 312 A; 244 C; 240 G; 227 T; 0 other;

Query Match 78.5%; Score 527; DB 24; Length 1023;
Best Local Similarity 87.8%; Pred. No. 2.2e-156;
Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Oy 1 ACAACGAGATTTGCCCTACTGATGAGAAAGCTAAACGAAATTCAGAAAGGACATTA 60
Db 215 ACAACGAGATTTGCCCTACTGATGAGAAAGCTAAACGAAATTCAGAAAGGACATTA 274
Oy 61 CATCAACTATGATGATTAAGCTCTGCTTGGAAAGAAACATTAAGAAAGATATGCTT 120
Db 275 CGTACAACTATGATGATTAAGCTCTGCTTGGAAAGAAACATTAAGAAAGATATGCTT 334
Oy 121 TTCTCTATTAAGAAAGGCTAGTGTCTGTAAACAAACCTACCTTACACAGCATATACAG 180
Db 335 TTCTCTATTAAGAAAGGCTAGTGTCTGTAAACAAACCTACCTTACACAGCATATACAG 394
Oy 181 CTGAGAGCAGATGATGTTTTCAGGGAACCTTTGTGTCGTTCCAGTCAACCTTACA 240
Db 395 ATGGAGAGCAGATGATGTTTTCAGGGAACCTTTGTGTCGTTCCAGTCAACCTTACA 454
Oy 241 CGCGTGTCAAGAGCTTGCTGATGTTGCTCCCTGCAACACCCCTGAGACATCCGTTAGAG 300
Db 455 CTGCTGTCAAGAGCTTGCTGATGTTATCCCTGCAACACCCCTGAGACATCCGTTAGAG 514
Oy 301 AGATTGATGAGCTGCTGATGCTTACACAGATGTAACGTCGCTGGAATGACAGAAAT 360
Db 515 AGATCGATGATGTTGTTGAGGTCTACACGACGTAACACCGCTGGAAGCGGAGAAAT 574
Oy 361 TCATTTTTCATGAGTGAATCTTCAATGCTGCTGACGTAACGTTCCCAAGAGGCTTGAAG 420
Db 575 TCATTTTTCATGAGTGAATCTTCAATGCTGCTGACGTAACGTTCCCAAGAGGCTTGAAG 634
Oy 421 ACATCCGCTGAGAGCGGAGCCCAAGTTGCTTTGGCTGATCGGGGACCAAGAGGACCA 480
Db 635 ACATCCGCTGAGAGCGGAGCCCAAGTTGCTTTGGCTGATCGGGGACCAAGAGGACCA 694
Oy 481 CGGTCAAGAGAGGACCAAACTGCGCTTATGACAGATGCTGCTTGAAGGACCAAAATATTG 540
Db 695 CGGTCAAGAGAGGACCAAACTGCGCTTATGACAGATGCTGCTTGAAGGACCAAAATATTG 754
Oy 541 TCAACTCTGAGTGTCTTCAATCAAACTCTGCTTTGATTTTCCAGAAAGCTTACAGTTGT 600
Db 755 TCAACTCTGAGTGTCTTCAATCAAACTCTGCTTTGATTTTCCAGAAAGCTTACAGTTGT 814
Oy 601 CTGAATGGAAGGCGCTGATGTCAGGACCACTTCAGTTCAATCATCATCATCA 655
Db 815 CTGAATGGAAGGCGCTGATGTCAGGACCACTTCAGTTCAATCATCATCATCA 869

RESULT 5
ABL61914
ID ABL61914 standard; DNA; 1023 BP.
XX
AC ABL61914;
XX
XX 15-MAY-2002 (first entry)
XX
DE Colon adenocarcinoma related gene sequence SEQ ID NO:251.
XX
KM Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KM stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KM cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KM gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.

20-SEP-2000; 2000US-234009P.
 20-SEP-2000; 2000US-234034P.
 20-SEP-2000; 2000US-234052P.
 22-SEP-2000; 2000US-234509P.
 22-SEP-2000; 2000US-234567P.
 25-SEP-2000; 2000US-234923P.
 25-SEP-2000; 2000US-234924P.
 25-SEP-2000; 2000US-235077P.
 25-SEP-2000; 2000US-235082P.
 25-SEP-2000; 2000US-235134P.
 25-SEP-2000; 2000US-235280P.
 26-SEP-2000; 2000US-235637P.
 26-SEP-2000; 2000US-235638P.
 27-SEP-2000; 2000US-235711P.
 27-SEP-2000; 2000US-235720P.
 27-SEP-2000; 2000US-235840P.
 27-SEP-2000; 2000US-235863P.
 28-SEP-2000; 2000US-236028P.
 28-SEP-2000; 2000US-236032P.
 28-SEP-2000; 2000US-236033P.
 28-SEP-2000; 2000US-236034P.
 28-SEP-2000; 2000US-236109P.
 28-SEP-2000; 2000US-236111P.
 29-SEP-2000; 2000US-236842P.
 29-SEP-2000; 2000US-236891P.
 02-OCT-2000; 2000US-237172P.
 02-OCT-2000; 2000US-237173P.
 02-OCT-2000; 2000US-237278P.
 02-OCT-2000; 2000US-237294P.
 02-OCT-2000; 2000US-237295P.
 02-OCT-2000; 2000US-237316P.
 03-OCT-2000; 2000US-237425P.
 03-OCT-2000; 2000US-237598P.
 03-OCT-2000; 2000US-237604P.
 03-OCT-2000; 2000US-237606P.
 03-OCT-2000; 2000US-237608P.
 01-NOV-2000; 2000US-244867P.
 01-NOV-2000; 2000US-245084P.
 (AVAL-) AVALON PHARM.
 Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 Soppet DR, Weaver Z;
 WPI; 2002-188264/24.
 Screening for anti-neoplastic agent involves exposing cells to a
 chemical agent to be tested for anti-neoplastic activity, and
 determining a change in expression of a gene of a signature gene set -
 Claim 1; SEQ ID 251; 44pp; English.
 The present invention describes a method (M1) for screening for an
 anti-neoplastic agent. The method involves exposing cells to a chemical
 agent to be tested for anti-neoplastic activity, determining a change in
 expression of at least one gene (I) of a signature gene set, where (I)
 comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 to ABL70110), or is at least 95% identical to (S), where a change in
 expression is indicative of anti-neoplastic activity. (I) has cytostatic
 activity and can be used in gene therapy. M1 can be used for screening
 an anti-neoplastic agent, and can be used for producing a product which
 is the data collected with respect to the anti-neoplastic agent as a
 result of M1, and the data is sufficient to convey the chemical
 structure and/or properties of the agent. M1 can be used in the
 treatment of cancer such as colon, breast, stomach, lung, thyroid,
 oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 carcinoma, papillary carcinoma and Wilm's tumour.
 Sequence 1023 BP; 312 A; 244 C; 240 G; 227 T; 0 other;
 Query Match 78.5%; Score 527; DB 24; Length 1023;

Best Local Similarity 87.8%; Pred. No. 2.2e-156;
 Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
 QY 1 ACAACAGGATCTGCCCATCTACTGATGGAGAGCTAAACCGNAATTCAAGAAAGGCATAA 60
 DB 215 ACAACAGGATCTGCCCATCTACTGATGGAGAGCTAAACCGNAATTCAAGAGAGGCATAA 274
 QY 61 CATACAACTATGTGATTAGCTCTCGCTTGGAGAAACACATATAAAGAACAGTATGCT 120
 DB 275 CGTACAACCTATGTGATTAGCTCTCGCTTGGAGAAACACATATAAAGAACATATGCT 334
 QY 121 TTCTCTATAAAGAAAGCTAGTCTGTAAACAAAGCTACCTCTACACGACTATCAGG 180
 DB 335 TTCTCTATAAAGAAAGCTAGTCTGTAAACAAAGCTATCCTACCTACCTATCAGG 394
 QY 181 CTGGAGACGACATGTTTCCAGGAAACCTTTGTGTCTGTTCCAGTCAACCTTAC 240
 DB 395 ATGGAGACGACATGTTTCCAGGAGCCCTTTGTGTCTGTTCCAAATCTCCCCACA 454
 QY 241 CGCTGTCAAGGACTTCGTGATTGTCCCTCTGCACACACCCCTGAGACATCCGTTAGAG 300
 DB 455 CTGCTGTCAAGACTTCGTGATTATCCCTCTGCACACACCCAGAGACATCCGTTAAG 514
 QY 301 AGATTGATGAGCTGCTGATGTCTACACAGATGTGAACGTCGCTGGAATGACAGAAAT 360
 DB 515 AGATCGATGAGTTGGTTGAGGTCTACACGACGTGAACACACCGCTGGAGGCGGAAT 574
 QY 361 TCATTTTCATGGTGACATTCATGCTGCTGAGTACGCTCCCAAGAGGCTTGAAGG 420
 DB 575 TCATTTTCATGGTGACATTCATGCTGCTGAGTACGCTCCCAAGAGGCTTGAAGG 634
 QY 421 ACATCCGCTGAGGACGACCCCAAGTTCTGTTGGCTGATCGGGACCAAGAGGACACCA 480
 DB 635 ACATCCGCTGAGGACTGACCCAGGTTTGTGCTGATCGGGACCAAGAGGACACCA 694
 QY 481 CGGTCAAGAGACACAACTCGGCTATGACAGGATCGCTTAGAGGACAAATATTG 540
 DB 695 CGGTGAAGAGAGACCAACTGTGCATATGACAGGATTTGTCTTAGAGGACAAATCG 754
 QY 541 TCAACTCTGCTGCTCTCAATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGTTCT 600
 DB 755 TCAGTTCTGTTTCTCCCAAGTCAAAAGTGTGTTTACCTTCCAGAAAGCTTACAGCTGA 814
 QY 601 CTGAATCGAAGGCTTGGATGTGACGACCACTTTCCAGTTTCATCATCATCA 655
 DB 815 CTGAAGAGGAGGCTTGGATGTGACGACCACTTTCCAGTTTCATCATCA 869
 RESULT 6
 ID ABL64458 standard; DNA; 1023 BP.
 XX ABL64458;
 AC ABL64458;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Stomach cancer related gene sequence SEQ ID NO:2795.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200194629-A2.
 PN
 XX
 PD 13-DEC-2001.
 XX
 XX
 PF 30-MAY-2001; 2001WO-US10838.
 XX
 XX 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.

PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
XX (AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppe DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
XX
PS Claim 1; SEQ ID 2795; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer.
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
XX Sequence 1023 BP; 312 A; 244 C; 240 G; 227 T; 0 other;

Query Match 78.5%; Score 527; DB 24; Length 1023;
Best Local Similarity 87.8%; Pred. No. 2.2e-156;
Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 1 ACAACAGGATCTGCCCATCTAGTATGAGAAAGCTTAACCGAATTTCAAGAAAGGCATTA 60
DB 215 ACAACAGGATCTGCCCATCTAGTATGAGAAAGCTTAACCGAATTTCAAGAGGCATTA 274
QY 61 CATACAACTATGATTAGTCTCGCTTGAGAAACACATATAAAGACAGATGCTT 120
DB 275 CGTAACTATGATTAGTCTCGCTTGAGAAACACATATAAAGACAGATGCTT 334
QY 121 TTCTCTATAAAGAAAGCTAGTGTCTGTAAACAAAGCTACCTTACACGATATCAGG 180
DB 335 TTCTCTATAAAGAAAGCTAGTGTCTGTAAAGAGAGATTATCACTACATGATCATCAGG 394
QY 181 CTGAGAGCGCAGATGTGTTTTCCAGGAAACCTTTGTGTGTGTTCCAGTACACCTTACA 240
DB 395 ATGAGAGCGCAGATGTGTTTTCCAGGAGCCCTTTGTGTGTGTTCCAGTACACCTTACA 454
QY 241 CCGCTGTCAAGACCTTGCTGATTTGCCCCCTGCACACACCCTGAGACATCCGTTAGAG 300
DB 455 CTGCTGTCAAGACCTTGCTGATTTATCCCCCTGCACACACCCTGAGACATCCGTTAAG 514
QY 301 AGATTGATGAGCTGCTGATGCTTACACAGATGTGAACCTGCTGAATGACAGAAATT 360
DB 515 AGATCGATGAGTGTGAGGTCTACACGACGTAACACCCGCTGAGAGCGGAGAAATT 574
QY 361 TCATTTTCATGAGGAGCTTCAATGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGG 420
DB 575 TCATTTTCATGAGGAGCTTCAATGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGG 634
QY 421 ACATCCGCTGAGAGCGACGCCCAAGTTGCTTGGCTGATGCGGAGCAAGAGGACACCA 480
DB 635 ACATCCGCTGAGAGCTGACGCCCAAGTTGCTTGGCTGATGCGGAGCAAGAGGACACCA 694
QY 481 CGGTCAAGAGAGCAAACTGCGCTTATGACAGATGCTGTAGAGACAAATATTG 540
DB 695 CGGTCAAGAGAGCAAACTGCGCTTATGACAGATGCTGTAGAGACAAATATTG 754
QY 541 TCAACTCTGCTGCTGCTCAATCAACCTGCTTGAATTCAGAAAGCTTACAGGTTGT 600
DB 755 TCAAGTCTGCTGCTTCCCAAGTCAACAGTGTGTTGACTTCCAGAAAGCTTACAGCTGA 814
QY 601 CTGAATCGAAGCCCTGATGTACGACCACTTCCAGTTCATCATCATCATCA 655
DB 815 CTGAAGAGAGAGCCCTGATGTACGACCACTTCCAGTTCATCATCATCATCA 869
RESULT 7
ABL64961
ID ABL64961 standard; DNA; 1023 BP.
XX
XX ABL64961;
XX
XX 15-MAY-2002 (first entry)
XX
XX Lung cancer related gene sequence SEQ ID NO:3298.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
XX
XX Homo sapiens.
XX
XX W0200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US10838.
XX

PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233133P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 03-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
PS Claim 1; SEQ ID 3298; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.

XX
SQ Sequence 1023 BP; 312 A; 244 C; 240 G; 227 T; 0 other;
Query Match 78.5%; Score 527; DB 24; Length 1023;
Best Local Similarity 87.8%; Pred. No. 2.2e-156;
Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 1 ACAACAGGATCTGCCCATCTACTGATGGAGAGCTAAACGAAATTCAGAAAAGGCATAA 60
Db 215 ACAACAGGATCTGCCCATCTACTGATGGAGAGCTAAACGAAATTCAGAGAGAGGCATAA 274
QY 61 CATACAACTATGTAGTACTCTCCCTTGGAGAGAAACACATATAAAGAACAGTAGTCCT 120
Db 275 CGTCACACTATGTAGTACTCTCCCTTGGAGAGAAACACATATAAAGAACAGTAGTCCT 334
QY 121 TTCTCTATAAAGAAAAGCTAGTGTCTGTAAACAAAGCTTACCTTACCACGACTATCAGG 180
Db 335 TTCTCTACAGGAAAAGCTGGTGTCTGTGAGAGGAGTTATCACTACCATGACTATCAGG 394
QY 181 CTGGAGACGCAGATGTGTTTTCCAGGGAACCCCTTTGTGTCTGTGGTTCCAGTCAACCTACA 240
Db 395 ATGGAGACGCAGATGTGTTTTCCAGGAGGCCCTTTGTGTCTGTGGTTCCAATCTCCCCACA 454
QY 241 CCGCTGTCAAGGACTTGTGTGATTTGCCCTCTGCAACACCCCTTGAGACATCCGTTAGAG 300
Db 455 CTGCTGTCAAAGACTTGTGTGATTTGCCCTCTGCAACACCCCTTGAGACATCCGTTAGAG 514
QY 301 AGATTGATGAGCTGGCTGATGCTACACAGATGTGAAACGCTGCGTGGATGCAGAGATT 360
Db 515 AGATCGATGAGTTGGTTGAGGTTACACGGAGCTGAAACACCGCTGGAGGCGGAGATT 574
QY 361 TCATTTTTCATGGTGACTTCAATGCTGCTGAGCTAGCTCCCAAGAGGCTTGGAGG 420
Db 575 TCATTTTTCATGGTGACTTCAATGCTGCTGAGCTAGCTCCCAAGAGGCTTGGAGG 634
QY 421 ACATCCGCTGAGGACGGAACCCAAAGTTGCTTTGGCTGATCGGGGACCAAGAGGACACCA 480
Db 635 ACATCCGCTTGAAGACTGACCCAGGTTTGTGGCTGATCGGGGACCAAGAGGACACCA 694
QY 481 CGGTCAAGAAGACACAAACTGCGCTATGACAGGATCGTCTTAGAGGACAAATATTG 540
Db 695 CGTGAAGAAGACACCAACTGTCATATGACAGGATTTGTCTTAGAGGACAAAGAAATCG 754
QY 541 TCAACTCTGGTGGTCTCTCAATCAAAACCTCGTCTTTGATTTCCAGAAAAGCTTACAGGTTGT 600
Db 755 TCAGTTCTGTGTTCCCAAGTCAACACTGTTTGTGACTTCCAGAAAAGCTTACAGGTTGA 814
QY 601 CTGAATCGAAGGCCCTGATGTACAGGACCACTTTTCCAGTTTCATCATCATCA 655
Db 815 CTGAAGAGAGGAGGCCCTGGATGTACAGGACCACTTTTCCAGTTGAATTTAAACTACA 869
RESULT 8
AAT74076
ID AAT74076 standard; cDNA; 1079 BP.
XX
AC AAT74076;
XX
DT 29-JAN-1998 (first entry)
XX
DE Human LS-DNase nucleotide sequence.
XX
KW DNase; actin; DNA viscoelasticity; systemic lupus erythematosus;
KW cystic fibrosis; meningitis; pulmonary disease; gene therapy;
KW recombinant preparation; DNA-hydrolytic activity; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 71..988
FT sig_peptide /*tag= a
FT 71..130
FT /*tag= b

CC Also included are modulating (M2) CA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection, and
CC parasitic infection; protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1108 BP; 329 A; 261 C; 271 G; 247 T; 0 other;

Query Match 78.3%; Score 525.4; DB 24; Length 1108;
Best Local Similarity 87.6%; Pred. No. 7.5e-156;
Matches 574; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1 ACAACAGGATCTGCCCATCTGATGAGAGCTAACCGAAATTCAGAAAGGCATAA 60
DB 283 ACAACAGGATCTGCCCATCTGATGAGAGCTAACCGAAATTCAGAGAGGCATAA 342
QY 61 CATACAACTATGTAGTCTCGCTTGGAGAGAACATATAAGAACAGTATGCTT 120
DB 343 CGTACAACTATGTAGTCTCGCTTGGAGAGAACATATAAGAACAGTATGCTT 402
QY 121 TTCTCTATAAGAAAGCTAGTCTGTAAACAAAGCTACCTACCAAGCTATCAGG 180
DB 403 TTCTCTATAAGAAAGCTAGTCTGTAAACAAAGCTATCCTACCAAGCTATCAGG 462
QY 181 CTGGAGACGACATGTGTTTCCAGGAAACCTTTTGTGCTGTTTCCAGTCAACCTACA 240
DB 463 ATGGAGACGACATGTGTTTCCAGGAGCCCTTTTGTGCTGTTTCCATCTCCCCACA 522
QY 241 CCGCTCTAAGGACTTGTGATGTTCCCTGTCACACCAACCTCTGAGACATCGTTPAGAG 300
DB 523 CTGCTCTAAGGACTTGTGATGTTATCCCTGTCACACCAACCTCTGAGACATCGTTPAGG 582
QY 301 AGATTGATGAGCTGCTGATCTACACAGATGTGAACGCTGCTGATGACAGAAAT 360
DB 583 AGATGATGAGTGTGTTGAGTCTACACGAGCGTGAACACCGCTGGAAGCGGGAAT 642
QY 361 TCATTTTCATGGTGACTTCAATGCTGGCTGACGTACGTCCTCCCAAGAGGCTGGAAGG 420
DB 643 TCATTTTCATGGTGACTTCAATGCTGGCTGACGTACGTCCTCCCAAGAGGCTGGAAGA 702
QY 421 ACATCCGCTGAGGACGACCCCAAGTCTCTTTGGCTGATCGGGGACCAAGAGCACCA 480
DB 703 ACATCCGCTGAGGACGACCCCAAGTCTCTTTGGCTGATCGGGGACCAAGAGCACCA 762
QY 481 CGGTCAAGAGACCAAACTGCGCTTATGACAGGATCGTCTTAGAGGACAAATATTG 540
DB 763 CGGTGAAGAAGACCAAACTGTCATATGACAGGATTTGCTTAGAGGACAAAGAAATCG 822

QY 541 TCAACTCTGGTGGTCTCTCAATCAAAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGT 600
DB 823 TCAGTTCTCTGTTTCCCAAGTCAAAACAGTGTGTTTGTGACTTCCAGAAAGCTTACAGCTGA 882
QY 601 CTGAATCGAAGGCGCTCGATGTCAGGACCACTTCCAGTTCATCATCATCATCA 655
DB 883 CTGAAGAGAGGAGCGCTCGATGTCAGGACCACTTCCAGTTCATCATCATCATCA 937
RESULT 10
AAS17901
ID AAS17901 standard; cDNA; 556 BP.
XX
AC AAS17901;
XX
DT 26-MAR-2002 (first entry)
XX
DE Partail cDNA encoding human fertility-associated antigen (FAA), HCl.
KW Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome;
KW reproductive fitness; single nucleotide polymorphism; SNP; human;
KW HCl; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..555
FT /*tag= a
FT /product= "Human FAA"
FT /note= "Human fertility-associated antigen, HCl"
FT /partial
FT /note= "No start or stop codon given"
FT /transl_except= (pos:1..3, aa:KVIRKCDIILVWEIKDS)
FT /transl_except= (pos:253..255, aa:S)
XX WO200176529-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US10802.
XX
PR 07-APR-2000; 2000US-195225P.
XX (ZHAN/) ZHANG H M.
PA (AXEL/) AX R L.
XX
PI Zhang HM, Ax RL;
XX
DR WPI; 2002-066307/09.
DR P-PSDB; AAU11517.
XX
PT Novel human or bovine fertility-associated antigen useful for
PT stabilising sperm cell acrosome and increasing fertility of a male
XX
PS Claim 1; Fig 2A-E; 54pp; English.
XX
CC The invention describes a novel isolated human fertility-associated
CC antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful
CC for increasing the stability of a sperm cell acrosome and for increasing
CC the fertility of a human male by administering FAA. Detecting single
CC nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful
CC for assaying fertility by detecting the presence or absence of a FAA SNP
CC in the mammal and correlating the presence or absence with the fertility
CC of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the
CC specification. FAA SNP is also useful for determining the reproductive
CC fitness of a human or bovine, by determining the nucleotide sequence of
CC the FAA SNP, quantifying the fertility of more than one mammal containing
CC the FAA SNP and correlating the frequency of the FAA SNP to the
CC reproductive fitness of the mammals. FAA improves the integrity of sperm
CC membranes and increases the capacitation of sperm derived from either
CC fertile or infertile humans. Early genetic identification of infertility
CC improves the prognosis for subsequent attempts at fertilisation and

CC facilitates early intervention to determine whether the individual may
CC benefit from fertility treatments to avoid costly and/or emotional
CC problems with attempted inseminations. This sequence encodes the human
CC fertility-associated antigen (FAA), HCl, one of 4 partial prostate CDNA
CC clones of the novel FAA gene described in the method of the invention.
XX

SO Sequence 556 BP; 159 A; 130 C; 142 G; 125 T; 0 other;

Query Match 77.3%; Score 518.4; DB 24; Length 556;
Best Local Similarity 96.2%; Pred. No. 8.5e-154;
Matches 531; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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OY 1 ACAAGAGATGCGCCCACTAGTGAAGAGCTAAAGCAATTCAGAAAGGATTA 60
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Db 5 ACAAGAGATGCGCCCACTAGTGAAGAGCTGAACGAAATTCAGAAAGGATTA 64
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OY 61 CATACAACTATGTATGATCTCCGCTTGAAGAAACATATTAAGACATATGCTT 120
   |||
Db 65 CGTACAACTATGTATGATCTCCGCTTGAAGAAACATATTAAGACATATGCTT 124
   |||
OY 121 TTCTCTATAAGAAAGCTAGTGTCTGTAACAAAGCTACCTTACACGACTATCAG 180
   |||
Db 125 TTCTCTACAGAAAGCTAGTGTCTGTAAGAGAGATATACATACATATCAGG 184
   |||
OY 181 CTGAGAGCGCAATGTGTTTCCAGGAAACCTTTGTGTCTGTCCAGTACCCCTACA 240
   |||
Db 185 ATGGAGAGCGCAATGTGTTTCCAGGAAACCTTTGTGTCTGTCCAGTACCCCTACA 244
   |||
OY 241 CCGCTGTCAAGACTTGTGATGTTCCCTGACACACACCCCTGAGACATCCGTTAG 300
   |||
Db 245 CCGCTGTCAAGACTTGTGATGTTCCCTGACACACACCCCTGAGACATCCGTTAG 304
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OY 301 AGATTGATGAGCTGCTGTATGTTCTACACAGATGTAAGCTGCTGGAATGACAGATT 360
   |||
Db 305 AGATTGATGAGCTGCTGTATGTTCTACACAGATGTAAGCTGCTGGAATGACAGATT 364
   |||
OY 361 TCATTTTATGAGGATGACTTCATGCTGCTGAGCTAGCTCCCAAGAGGCTGGAAG 420
   |||
Db 365 TCATTTTATGAGGATGACTTCATGCTGCTGAGCTAGCTCCCAAGAGGCTGGAAG 424
   |||
OY 421 ACATCCGCTGAGAGACGACCCCAAGTTGCTGTATCGGGAGCCAAAGAGACACCA 480
   |||
Db 425 ACATCCGCTGAGAGACGACCCCAAGTTGCTGTATCGGGAGCCAAAGAGACACCA 484
   |||
OY 481 CCGTCAAGAGACCAAACTGCGCTATGACAGATGCTGTTAGAGACAAATATTG 540
   |||
Db 485 CCGTCAAGAGACCAAACTGCGCTATGACAGATGCTGTTAGAGACAAATATTG 544
   |||
OY 541 TCAACTCTGTG 552
   |||
Db 545 TCAACTCTGTG 556
   |||
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RESULT 11

ID AAT17733 standard; cDNA, 1208 BP.

AC AAT17733;

DT 17-OCT-1996 (first entry)

DE Deoxyribonuclease, DNase-gamma cDNA.

KX Deoxyribonuclease; DNase-gamma; selective cleavage; linker;

KM chromatin DNA; cell nucleus; 3'-hydroxy; 5'-phosphate; apoptosis;

KW carcinogenesis; AIDS development; diagnosis; prevention;

XX treatment; cancer; autoimmune disease; viral infections; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 12..944
FT CDS
FT /*tag= a

/note= "GAT codon comprising bases 837-839 has
no corresponding amino acid in AAR94021"

MO9607735-A1.

14-MAR-1996.

06-SEP-1995; 95WO-JP01775.

06-SEP-1994; 94JP-0239518.

(TANU/) TANUMA S.

Tanuma S;

WPI; 1996-171610/17.

P-PSDB; AAR94021.

PT DNase which selectively cuts linker region of chromatin DNA -
PT useful in diagnosis, treatment and prevention of cancer, autoimmune
PT diseases, viral infections, etc.

PS Claim 4; Pages 55-57; 75pp; Japanese.

CC The present sequence encodes the deoxyribonuclease, DNase-gamma,
CC which is able to selectively cleave the linker part of chromatin
CC DNA. DNase-gamma has a mol. wt. of 32000 by SDS-PAGE, or 30000 by
CC gel filtration, an optimum pH of 5.6, is found in the cell nucleus,
CC is not dependent on divalent cations, has a Zn(2+) inhibition
CC IC(50) > 1mM and leaves 3'-OH and 5'-P termini after cleavage. The
CC DNase can be used at a mol. level to resolve the control
CC mechanisms of carcinogenesis, the autoimmune system and AIDS
CC development. It can also be used in the diagnosis, prevention and
CC treatment of cancer, autoimmune disease, viral infections, etc.,
CC and as an apoptosis control agent.

SO Sequence 1208 BP; 319 A; 304 C; 282 G; 303 T; 0 other;

Query Match 71.5%; Score 479.6; DB 17; Length 1208;
Best Local Similarity 85.0%; Pred. No. 2.6e-141;
Matches 549; Conservative 0; Mismatches 94; Indels 3; Gaps 1;

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OY 1 ACAAGAGATGCGCCCACTAGTGAAGAGCTAAAGCAATTCAGAAAGGATTA 60
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Db 217 ACAAGAGATGCGCCCACTAGTGAAGAGCTAAAGCAATTCAGAAAGGATTA 64
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OY 61 CATACAACTATGTATGATCTCCGCTTGAAGAAACATATTAAGACATATGCTT 120
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Db 277 CATACAACTATGTATGATCTCCGCTTGAAGAAACATATTAAGACATATGCTT 124
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OY 121 TTCTCTATAAGAAAGCTAGTGTCTGTAACAAAGCTACCTTACACGACTATCAG 180
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Db 337 TTCTCTATAAGAAAGCTAGTGTCTGTAACAAAGCTACCTTACACGACTATCAG 184
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OY 181 CTGAGAGCGCAATGTGTTTCCAGGAAACCTTTGTGTCTGTCCAGTACCCCTACA 240
   |||
Db 397 CTGAGAGCGCAATGTGTTTCCAGGAAACCTTTGTGTCTGTCCAGTACCCCTACA 244
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OY 241 CCGCTGTCAAGACTTGTGATGTTCCCTGACACACCCCTGAGACATCCGTTAG 300
   |||
Db 457 CCGCTGTCAAGACTTGTGATGTTCCCTGACACACCCCTGAGACATCCGTTAG 304
   |||
OY 301 AGATTGATGAGCTGCTGTATGTTCTACACAGATGTAAGCTGCTGGAATGACAGATT 360
   |||
Db 517 AGATTGATGAGCTGCTGTATGTTCTACACAGATGTAAGCTGCTGGAATGACAGATT 364
   |||
OY 361 TCATTTTATGAGGATGACTTCATGCTGCTGAGCTAGCTCCCAAGAGGCTGGAAG 420
   |||
Db 577 TCATTTTATGAGGATGACTTCATGCTGCTGAGCTAGCTCCCAAGAGGCTGGAAG 424
   |||
OY 421 ACATCCGCTGAGAGACGACCCCAAGTTGCTGTATCGGGAGCCAAAGAGACACCA 480
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Db 637 ACATCCGCTGAGAGACGACCCCAAGTTGCTGTATCGGGAGCCAAAGAGACACCA 484
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FH Key Location/Qualifiers
FT 1..349
FT CDS /*tag= a
FT /product= "Human FFA"
FT /note= "Human fertility-associated antigen, HC2"
FT /partial
FT /note= "No start or stop codon given"
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XX WO200176529-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US10802.
XX
XX 07-APR-2000; 2000US-195225P.
XX
XX (ZHAN/) ZHANG H M.
XX (AXRL/) AX R L.
XX
XX Zhang HM, Ax RL;
XX
XX WPI; 2002-066307/09.
XX
XX P-PSDB; AAU11518.
XX
XX Novel human or bovine fertility-associated antigen useful for
XX stabilising sperm cell acrosome and increasing fertility of a male
XX
XX Claim 1; Fig 2A-E; 54pp; English.
XX
XX The invention describes a novel isolated human fertility-associated
XX antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful
XX for increasing the stability of a sperm cell acrosome and for increasing
XX the fertility of a human male by administering FAA. Detecting single
XX nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful
XX for assaying fertility by detecting the presence or absence of a FAA SNP
XX in the mammal and correlating the presence or absence with the fertility
XX of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the
XX specification. FAA SNP is also useful for determining the reproductive
XX fitness of a human or bovine, by determining the nucleotide sequence of
XX the FAA SNP, quantifying the fertility of more than one mammal containing
XX the FAA SNP and correlating the frequency of the FAA SNP to the
XX reproductive fitness of the mammals. FAA improves the integrity of sperm
XX membranes and increases the capacitation of sperm derived from either
XX fertile or infertile humans. Early genetic identification of infertility
XX improves the prognosis for subsequent attempts at fertilisation and
XX facilitates early intervention to determine whether the individual may
XX benefit from fertility treatments to avoid costly and/or emotional
XX clones of the novel FAA gene described in the method of the invention.
XX
XX Sequence 350 BP; 88 A; 91 C; 93 G; 78 T; 0 other;
XX
XX Query Match 51.9%; Score 348.4; DB 24; Length 350;
XX Best Local Similarity 99.7%; Pred. No. 5.1e-100;
XX Matches 349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX 203 CAGGAAACCCCTTGTGCTGCTTCCAGTACCTACACCGCTGCAAGAGACTTGAT 262
XX 1 CAGGAAACCCCTTGTGCTGCTTCCAGTACCTACACCGCTGCAAGAGACTTGAT 60
XX
XX 263 TGTCCCTCGACACACCCCTGAGACATCCGTTAGAGATTGATGAGCTGGAT 322
XX 61 TGTCCCTCGACACACCCCTGAGACATCCGTTAGAGATTGATGAGCTGGAT 120
XX
XX 323 CTACACAGATGTGAAGCTGCTGGAATGACAGAAATTCATTTCATGGGAGACTTCAA 382
XX 121 CTACACAGATGTGAAGCTGCTGGAATGACAGAAATTCATTTCATGGGAGACTTCAA 180
XX
XX 383 TGTCTGGCTGACACTGCTCCCAAGAGGCTGGAAGGACATCGCCTGAGAGCGGACCC 442
XX 181 TGTCTGGCTGACACTGCTCCCAAGAGGCTGGAAGGACATCGCCTGAGAGCGGACCC 240

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OY 443 CAAGTCTGTTGGCTGATCGGGGACCAAGAGACACCGGTCAAGAGACCAACTG 502
OY |||||
DB 241 CAAGTCTGTTGGCTGATCGGGGACCAAGAGACACCGGTCAAGAGACCAACTG 300
OY 503 CGCCTATGACAGATCGTGTCTTAAGAGCAAAATATTGTCAACTCTGATG 552
OY |||||
DB 301 CGCCTATGACAGATCGTGTCTTAAGAGCAAAATATTGTCAACTCTGATG 350

RESULT 14
AA517903
ID AA517903 standard; cDNA; 350 BP.
XX
XX AA517903;
XX
XX 26-MAR-2002 (first entry)
XX
XX partial cDNA encoding human fertility-associated antigen (FAA), HC3.
XX
XX Fertility-associated antigen, FAA; antifertility; sperm cell acrosome;
XX reproductive fitness; single nucleotide polymorphism, SNP; human;
XX HC3; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 2..349
XX FT /*tag= a
XX FT /product= "Human FFA"
XX FT /note= "Human fertility associated antigen, HC3"
XX FT /partial
XX FT /note= "No start or stop codon given"
XX FT /transl_except= (pos:251..253, aa: Arg)
XX
XX WO200176529-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US10802.
XX
XX 07-APR-2000; 2000US-195225P.
XX
XX (ZHAN/) ZHANG H M.
XX (AXRL/) AX R L.
XX
XX Zhang HM, Ax RL;
XX
XX WPI; 2002-066307/09.
XX
XX P-PSDB; AAU11519.
XX
XX Novel human or bovine fertility-associated antigen useful for
XX stabilising sperm cell acrosome and increasing fertility of a male
XX
XX Claim 1; Fig 2A-E; 54pp; English.
XX
XX The invention describes a novel isolated human fertility-associated
XX antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful
XX for increasing the stability of a sperm cell acrosome and for increasing
XX the fertility of a human male by administering FAA. Detecting single
XX nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful
XX for assaying fertility by detecting the presence or absence of a FAA SNP
XX in the mammal and correlating the presence or absence with the fertility
XX of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the
XX specification. FAA SNP is also useful for determining the reproductive
XX fitness of a human or bovine, by determining the nucleotide sequence of
XX the FAA SNP, quantifying the fertility of more than one mammal containing
XX the FAA SNP and correlating the frequency of the FAA SNP to the
XX reproductive fitness of the mammals. FAA improves the integrity of sperm
XX membranes and increases the capacitation of sperm derived from either
XX fertile or infertile humans. Early genetic identification of infertility
XX improves the prognosis for subsequent attempts at fertilisation and
XX facilitates early intervention to determine whether the individual may
XX benefit from fertility treatments to avoid costly and/or emotional

```

CC problems with attempted inseminations. This sequence encodes the human
CC fertility-associated antigen (FAA), HC3, one of 4 partial prostate cDNA
CC clones of the novel FAA gene described in the method of the invention.
XX
SQ Sequence 350 BP; 89 A; 93 C; 94 G; 74 T; 0 other;

Query Match 46.9%; Score 314.8; DB 24; Length 350;
Best Local Similarity 93.7%; Pred. No. 2.3e-89;
Matches 328; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 203 CAGGGAACCTTTGTGCTGTTCCAGTCACCTACCGCTGTCAAGGACTTCCTGAT 262
DB 1 CAGGAGACCTTTGTGCTGTTCCAAATCTCCACACTGCTGTCAAGACTTCCTGAT 60
QY 263 TGTCCCTCCGACACACCCCTGAGACATCCGTTAGAGAGATTGATGAGCTGCTGAT 322
DB 61 TATCCCTCCGACACACCCAGAGACATCCGTTAAGGAGATCGATGAGTTGTTGAGGT 120
QY 323 CTACACAGATGTGAACGTCGCTGGAATCGAGAGATTTCATTTTCATGGGTGACTTCAA 382
DB 121 CTACACGAGCGTGAACACCGCTGGAAGCGGAGAAATTTTCATTTTCATGGGTGACTTCAA 180
QY 383 TGTGCTGCTGAGTACGTCCTCCCAAGAGCGCTGGAAGGACATCCGCTGAGGACGACCC 442
DB 181 TGTGCTGCTGAGTACGTCCTCCCAAGAGCGCTGGAAGGACATCCGCTGAGGACGACCC 240
QY 443 CAAGTTTCGTTTGGCTGATCGGGACCAAGAGGACACACCGGTCAAGAGAGACACAACTG 502
DB 241 CAAGTTTCGTTTGGCTGATCGGGACCAAGAGGACACACCGGTCAAGAGAGACACAACTG 300
QY 503 CGCCTATGACAGATCGTCTGTAGAGGACAAAATATTTGCAACTCTGGTG 552
DB 301 CGCCTATGACAGATCGTCTGTAGAGGACAAAATATTTGCAACTCTGGTG 350

RESULT 15
AAS17904
ID AAS17904 standard; cDNA; 349 BP.
XX
AC AAS17904;
XX
DT 26-MAR-2002 (first entry)
XX
DE Partial cDNA encoding human fertility-associated antigen (FAA), HC4.
XX
KW Fertility-associated antigen; FAA; antiinfertility; sperm cell acrosome;
KW reproductive fitness; single nucleotide polymorphism; SNP; human;
XX HC4; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..348
FT /*tag= a
FT /product= "Human FAA"
FT /note= "Human fertility-associated antigen, HC4"
FT /partial
FT /note= "No start or stop codon given"
FT /transl_except= (pos: 11..12, aa:Phe)
FT /note= "This codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
XX
PN W0200176529-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US10802.
XX
PR 07-APR-2000; 2000US-195225P.
XX
PA (ZHAN/) ZHANG H M.
PA (AXRL/) AX R L.
XX

PI Zhang HM, Ax RL;
XX WPI; 2002-066307/09.
DR P-PSDB; AAU11520.
XX
XX Novel human or bovine fertility-associated antigen useful for
PT stabilising sperm cell acrosome and increasing fertility of a male -
PT
PS Claim 1; Fig 2A-E; 54pp; English.
XX
CC The invention describes a novel isolated human fertility-associated
CC antigen (FAA) and a bovine FAA polypeptide. Human or bovine FAA is useful
CC for increasing the stability of a sperm cell acrosome and for increasing
CC the fertility of a human male by administering FAA. Detecting single
CC nucleotide polymorphisms (SNPs) of the human or bovine FAA gene is useful
CC for assaying fertility by detecting the presence or absence of a FAA SNP
CC in the mammal and correlating the presence or absence with the fertility
CC of the mammal. The FAA SNPs are chosen from FAA SNPs 1-34 given in the
CC specification. FAA SNP is also useful for determining the reproductive
CC fitness of a human or bovine, by determining the nucleotide sequence of
CC the FAA SNP, quantifying the fertility of more than one mammal containing
CC the FAA SNP and correlating the frequency of the FAA SNP to the
CC reproductive fitness of the mammals. FAA improves the integrity of sperm
CC membranes and increases the capacitation of sperm derived from either
CC fertile or infertile humans. Early genetic identification of infertility
CC improves the prognosis for subsequent attempts at fertilisation and
CC facilitates early intervention to determine whether the individual may
CC benefit from fertility treatments to avoid costly and/or emotional
CC problems with attempted inseminations. This sequence encodes the human
CC fertility-associated antigen (FAA), HC4, one of 4 partial prostate cDNA
XX clones of the novel FAA gene described in the method of the invention.
SQ Sequence 349 BP; 89 A; 91 C; 93 G; 76 T; 0 other;

Query Match 44.8%; Score 300.5; DB 24; Length 349;
Best Local Similarity 91.6%; Pred. No. 7.3e-85;
Matches 318; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 206 GGAACCCCTTTGTGGTCTGGTCCAGTCAACCTTACACCGCTGTCAAGGACTTCGTGATTC 265
DB 3 GGGAGCCCTTTGTGGTCTGGTCCATCTCCCCACACTGCTGTCAAGAGACTTCGTGATTA 62
QY 266 CCCCTGTCACACCCCTCGAGACATCCGTTAGAGAGATTGATGAGCTGGCTGTGTTA 325
DB 63 CCCCTGTCACACCCCTCGAGACATCCGTTAAGGAGATCGATGAGTTGGTTGAGGTCTA 122
QY 326 CACAGATGTGAACGTCGCTGGAATCGAGAGAAATTTTCATTTTCATGGGTGACTTCAATGC 385
DB 123 CACGGACGTGAACACCCGCTGGAAGCGGAGAAATTTTCATTTTCATGGGTGACTTCAATGC 182
QY 386 TGGCTGCAGCTACGTCCCAAGAGCGCTGGAAGGACATCCGCTGAGGACGACCCCAA 445
DB 183 CGGCTGCAGCTACGTCCCAAGAGCGCTGGAAGAGAAATTCGCTTGAGAGCTGACCCGAG 242
QY 446 GTTCGTTTGGCTGATCGGGGACCAAGAGGACACCAACCGTCAAGAGAGACACAACTGCGC 505
DB 243 GTTTCGTTTGGCTGATCGGGGACCAAGAGGACACCAACCGTCAAGAGAGACACAACTGCGC 302
QY 506 CTATGACAGGATCGTGTCTAGAGGACAAAATATTTGCAACTCTCTGGTG 552
DB 303 CTATGACAGGATCGTGTCTAGAGGACAAAATATTTGCAACTCTCTGGTG 349

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Job time : 201.384 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
7261.235 Million cell updates/sec

Title: US-09-905-114-3

Perfect score: 671

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Scoring table: IDENTITY NUC

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: em_estmu:*
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9: gb_est1:*
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26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528.6	78.8	890	9	AL546857
2	526.6	78.5	896	9	AL546432
C 3	518.8	77.3	931	9	AL571894
C 4	511	76.2	833	9	AL572037
C 5	463	69.0	506	10	AV607154
6	458	68.3	666	10	BE048177

C 7	432.6	64.5	642	10	AW543356
C 8	428.8	63.9	695	13	B1522352
C 9	425.4	63.4	825	12	BG867772
10	422.4	63.0	825	13	BG330136
11	415.4	61.9	628	13	B1460950
C 12	412.2	61.4	620	10	AW543802
C 13	407.8	60.8	784	9	A1927844
C 14	407	60.7	610	10	AW540389
15	406.4	60.6	668	10	AW915564
16	402	59.9	832	13	B1838188
C 17	387.6	57.8	634	9	A1660448
C 18	387	57.7	685	13	B1833952
19	377	56.2	759	12	BG534290
C 20	374.2	55.8	566	10	AW538998
21	363.4	54.2	981	14	BQ710632
C 22	352.4	52.5	613	10	AW779563
C 23	351.4	52.4	578	10	AW658627
C 24	351.2	52.3	527	10	AW539589
C 25	335.2	50.0	643	10	AW001760
C 26	329.8	49.2	714	12	BG566893
C 27	321	47.8	542	12	BF434855
28	320.8	47.8	855	12	BF237166
C 29	314.2	46.8	554	10	AW243180
C 30	313	46.6	555	9	A1434430
31	309.8	46.2	901	12	BF303508
C 32	309.2	46.1	487	9	A1194886
C 33	303.8	45.3	497	9	AA564572
34	291.2	43.4	586	13	BM489658
35	284.2	42.4	595	12	BG077563
C 36	283.8	42.3	433	12	BF911384
C 37	279.8	41.7	341	10	AW803005
C 38	276.6	41.2	511	9	A1271665
C 39	272.6	40.6	523	9	A1248904
40	267.6	39.9	522	14	BQ186387
C 41	264.6	39.4	536	9	AA707043
C 42	263.8	39.3	486	9	AA989198
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C 45	251.8	37.5	404	13	BM386137

ALIGNMENTS

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DEFINITION AL546857 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI026YK08 5
prime, mRNA sequence.
ACCESSION AL546857
VERSION AL546857.1 GI:12880381
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT)_primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>

BASE COUNT 250 a 215 c 220 g 204 t 1 others
ORIGIN

Query Match 78.8%; Score 528.6; DB 9; Length 890;
Best Local Similarity 87.9%; Pred. No. 4.3e-141;
Matches 576; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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DB 250 CATACACTATGTGATGTAGCTCTCGCTTGGAAAGAACATTAAGAACATGTGCTT 309
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DEFINITION AL546432 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1030YD20 5
ACCESSION AL546432
VERSION AL546432.1 GI:12879540
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 896)

AUTHORS Li, W.B., Gruber, C., Joesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/note="Vector: pCMVSPORT 6, Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT 249 a 217 c 226 g 203 t 1 others
ORIGIN

Query Match 78.5%; Score 526.6; DB 9; Length 896;
Best Local Similarity 87.6%; Pred. No. 1.6e-140;
Matches 574; Conservative 1; Mismatches 80; Indels 0; Gaps 0;

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QY 1 ACAACAGATCTGCCCTACTGATGAGAAAGCTTAAACGAAATTCAGAAAGGCATTA 60
DB 240 ACAACAGATCTGCCCTACTGATGAGAAAGCTTAAACGAAATTCAGAAAGGCATTA 299
QY 61 CATACACTATGTGATGTAGCTCTCGCTTGGAAAGAACATTAAGAACATGTGCTT 120
DB 300 CATACACTATGTGATGTAGCTCTCGCTTGGAAAGAACATTAAGAACATGTGCTT 359
QY 121 TTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACTACACGACTATCAG 180
DB 360 TTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACTACACGACTATCAG 419
QY 181 CTGAGACGCAAGATGTGTTTTCAGGGAAACCTTTGTGCTGTTCAGTACCTTCA 240
DB 360 TTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACTACACGACTATCAG 419
QY 420 ATGAGACGCAAGATGTGTTTTCAGGGAAACCTTTGTGCTGTTCAGTACCTTCA 479
DB 420 ATGAGACGCAAGATGTGTTTTCAGGGAAACCTTTGTGCTGTTCAGTACCTTCA 479
QY 241 CCGCTGTCAAGACTTCTGATGTGTCCTGACACACCCCTGAGCATCCGTTAAG 300
DB 480 CTGCTGTCAAGACTTCTGATGTGTCCTGACACACCCCTGAGCATCCGTTAAG 539
QY 480 CTGCTGTCAAGACTTCTGATGTGTCCTGACACACCCCTGAGCATCCGTTAAG 539
DB 539 CTGCTGTCAAGACTTCTGATGTGTCCTGACACACCCCTGAGCATCCGTTAAG 539
QY 301 AGATGATGAGCTGCTGATGTCTACACAGATGTGAAACGTCGCTGAAATGAGAAAT 360
DB 540 AGATGATGAGCTGCTGATGTCTACACAGATGTGAAACGTCGCTGAAATGAGAAAT 599
QY 540 AGATGATGAGCTGCTGATGTCTACACAGATGTGAAACGTCGCTGAAATGAGAAAT 599
DB 599 AGATGATGAGCTGCTGATGTCTACACAGATGTGAAACGTCGCTGAAATGAGAAAT 599
QY 361 TCATTTTCATGAGGATGACTTCAATGCTGTGCTGAGCTACGCTCCCAAGAGGCTTGAAG 420
DB 600 TCATTTTCATGAGGATGACTTCAATGCTGTGCTGAGCTACGCTCCCAAGAGGCTTGAAG 659
QY 421 ACATCCGCTGAGAGCGAAGCCCAAGTTCGTTGGCTGATCGGGAGCAAGAGGACACA 480
DB 660 ACATCCGCTGAGAGCGAAGCCCAAGTTCGTTGGCTGATCGGGAGCAAGAGGACACA 719
QY 481 CGGTCAAGAAAGACCAAACTGCGCTATGACAGATCGTGTGAGAGGACAAATATTG 540
DB 720 CGGTCAAGAAAGACCAAACTGCGCTATGACAGATCGTGTGAGAGGACAAATATTG 779
QY 541 TCAACTCTGTGTGCTCTCAATCAAACTTCGTTGATTTCCAGAAAGCTTACAGGTTGT 600
DB 780 TCAACTCTGTGTGCTCTCAATCAAACTTCGTTGATTTCCAGAAAGCTTACAGGTTGT 839
QY 601 CTGAATCGAAGGCGCTGATGTGACGAGCACTTCCAGTTTCATCATCATCATCA 655
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Db 840 CTGAAGAGGAGGCCCTGGATGTCAGCGACCACCTTTTCAGTTGAATTTAAACTACA 894

RESULT 3
AL571894/c
LOCUS
DEFINITION
AL571894 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI030YD20 3
prime, mRNA sequence.
AL571894
VERSION
AL571894.1 GI:12929641
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
AUTHORS
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..931
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI030YD20"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 209 a 219 c 225 g 271 t 7 others
ORIGIN
source
Query Match 77.3%; Score 518.8; DB 9; Length 931;
Best Local Similarity 86.7%; Pred. No. 2.9e-136;
Matches 568; Conservative 2; Mismatches 85; Indels 0; Gaps 0;

Qy 1 ACAACAGGATCTGCCCATCTGATGGAGAACTAAACGGAAATTCAGAAAAGGCATAA 60
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Db 752 ACAACAGGATCTGCCCATCTGATGGAGAACTAAACGGAAATTCAGAGAGGCATAA 693
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Qy 61 CATACAACTATGTGATTAGCTCTCGCTTGGAGAAACACATATAAAGAACAGTATGCT 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 692 CGTACACTATGTGATTGCTCTCGCTTGGAGAAACACATATAAAGAACATATGCT 633
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAAACAAAGCTACCTCTACCACGACTATCAGG 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 632 TTCTCTACAAGGAAAGGCTGGTGTCTGTGAAGAGGAGTTATNACTACCATGACTATCAGG 573
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 181 CTGGAGAGCCAGATGTTTCCAGGAAACCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 572 ATGGAGAGCGCAGATGTTTCCAGGAGGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 513
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Qy 241 CGCTGTCAAGGACCTTGTGATTGTCCTCCCTGCACACACCCCTCGAGACATCCGTTAGAG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 512 CTGCTGTCAAGACCTTGTGATTATCCCTCGACACACCCACCCAGAAACATCCGTTAAGG 453
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 301 AGATTGATGAGCTGCTGATGCTACACAGATGTGAACAGTGCCTGGAAATGCAGAGAAAT 360
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 452 AGATCGATGAGTTGTTGAGGTCTACACGAGCTGAACACACCGCTGGAGGGGAGAAAT 393
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 361 TCATTTTCATGGGTGACTTCAATGTGGCTGCGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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Db 392 TCATTTTCATGGGTGACTTCAATGCGGCTGCGAGTAGCGTCCCAAGAGGCGCTGGAAGA 333

Qy 421 ACATCCGCTGAGGACGGACCCCAAGTTTCGTTTGGCTGATCGGGACCAAGAGGACCA 480
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 332 ACATCCGCTTGAGAAGTACCCAGGTTTGTGCTGATCGGGACCAAGAGGACCA 273
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 481 CGGTCAAGAGAGACCAAACTCGGCTATGACAGGATCGTGTAGAGGACAAAATATTG 540
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 272 CGGTGAAGAGAGACCAAACTGTGCATATAACAGGATTGTGCTTAGAGGACAAAGATCG 213
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Qy 541 TCAACTCTGGTGGTCTCAATCAAACTCGTCTTTGATTCCAGAAAGCTTCAGGTTGT 600
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Db 212 TCAGTTCTGTTTCCCAAGTCAAAACAGTGTTCAGTTCCAGAAAGCTTCAGAGCTGA 153
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Qy 601 CTGAATCGAAGGCCCTGGATGTCAGCGACCACTTTCCAGTTTCATCATCATCATCA 655
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Db 152 CTGAAGAGGAGGCCCTGGATGTCAGCGACCACTTTCCAGTTGAATTTAAACTACA 98
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RESULT 4
AL572037/c
LOCUS
DEFINITION
AL572037 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI026YK08 3
prime, mRNA sequence.
AL572037
VERSION
AL572037.1 GI:12929919
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 833)
AUTHORS
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..833
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/clone="CSODI026YK08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 193 a 193 c 191 g 249 t 7 others
ORIGIN
source
Query Match 76.2%; Score 511; DB 9; Length 833;
Best Local Similarity 86.9%; Pred. No. 4.8e-136;
Matches 570; Conservative 2; Mismatches 83; Indels 1; Gaps 1;

Qy 1 ACAACAGGATCTGCCCATCTGATGGAGAACTAAACGGAAATTCAGAAAAGGCATAA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 760 ACAACAGGATCTGCCCATCTGATGGAGAACTAAACGGAAATTCAGAGGAGCATYA 701
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Qy 61 CATACAACTATGTGATTAGCTCTCGCTTGGAGAAACACATATAAAGAACAGTATGCT 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 700 CATACAACTATGTGATTAGCTCTCGCTTGGAGAAACACATATAAAGAACATATGCT 641
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 TTCTCTATAAAGAAAAGCTAGTGTCTGTAAAAACAAAGCTACCTCTACCACGACTATCAGG 180
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Db 640 TTCTCTACAGAGAAAGCTGTCTGTCTGTAAGAGAGATTATCATACATACATCAG 581
QY 181 CTGAGACGACAGATGTGTTTTCAGAGAAACCTTTGTGCTGTGTTCCAGTCACTTACA 240
Db 580 ATGAGACGACAGATGTGTTTTCAGAGAGACCTTTGTGCTGTGTTCCAGTCACTTACA 521
QY 241 CCGCTGTACAGACTTCCGATGTTTCCCTTCACACACACCTTCAGATCCGTTAGAG 300
Db 520 CTGCTGTACAAACCTTCGATTTATCCCTTCACACACACCTTCAGATCCGTTAGAG 461
QY 301 AGATTGATGAGCTGCTGATGTTCTACACAGATGTGAAACGTCGCTGGAATGAGAAATT 360
Db 460 AGATGATGAGCTGCTGATGTTCTACACAGATGTGAAACGTCGCTGGAATGAGAAATT 401
QY 361 TCATTTCATGAGGTTGATCTTCAATGCTGCTGAGCTATCCCAAGAGGCTTGAAAG 420
Db 400 TCATTTCATGAGGTTGATCTTCAATGCTGCTGAGCTATCCCAAGAGGCTTGAAAG 341
QY 421 ACATCCGCTGAGAGACGACCCCAAGTTCGTTGCTGATCGGGAGCCAAAGAGACACCA 480
Db 340 ACATCCGCTGAGAGACGACCCCAAGTTCGTTGCTGATCGGGAGCCAAAGAGACACCA 281
QY 481 CGGTCAAGAGAGACCAAACTGCGCTATGACAGATCGTCTTACAGACCAAAATATTG 540
Db 280 CGGTCAAGAGAGACCAAACTGCGCTATGACAGATCGTCTTACAGACCAAAATATTG 221
QY 541 TCACTCTGTGTTGCTCTCAATCAAACTTCGTTGATTTCAGAAAGCTTACAGATTGT 600
Db 220 TCAGTTCTGTGTTGCTCTCAAGTCAAAAGTTCGTTGATTTCAGAAAGCTTACAGTTGA 161
QY 601 CTGAATCCAGAGCCCTGATGTCAGCGAC-CACCTTCCAGTTCATCATCATATCA 655
Db 160 CTGAAGAGAGGCGCTGATGTCAGCGACCACTTCCAGTTGAATTAACTTACA 105

RESULT 5
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LOCUS AV607154 Bos taurus kidney fetus Bos taurus cDNA clone EIK1039505
DEFINITION 3', mRNA sequence.

ACCESSION AV607154
VERSION AV607154.1 GI:9737527
KEYWORDS EST.

SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 506)
TAKASUGA, A., HITOTSUNE, S., ITOH, R., JIHOZONO, A., SUZUKI, H., ABO, H.,
and SUGIMOTO, Y.
Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs

TITLE Nucleic Acids Res. 29 (22), E108 (2001)
JOURNAL MEDLINE 21570554
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odaiba, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES
Source
1..506
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="EIK1039B05"
/clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"

/lab_host="DH10B"
/note="Vector: pZL1; Site 1: SalI; Site 2: NotI; Poly A
was deleted from a NotI site"

BASE COUNT 124 a 126 c 129 g 126 t 1 others
ORIGIN

Query Match 69.0%; Score 463; DB 10; Length 506;
Best Local Similarity 97.7%; Pred. No. 2,66-122;
Matches 469; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 176 TCAGCTGAGAGACCAATGTTTTCAGAGAAACCTTTGTGCTGTGTTCCAGTCAACC 235
Db 506 TCAGCTGAGAGACCAATGTTTTCAGAGAAACCTTTGTGCTGTGTTCCAGTCAACC 447

QY 236 CTACACGCTGTCAAGACTTTCGATTTGCCCTTCACACACACCTTCGAGACATCCGT 295
Db 446 CTACACGCTGTCAAGACTTTCGATTTGCCCTTCACACACACCTTCGAGACATCCGT 387

QY 296 TAGAGATTTGATGAGCTGCTGATGTTCTACACAGATGTGAAACGTCGTAATGAGA 355
Db 386 TAGAGATTTGATGAGCTGCTGATGTTCTACACAGATGTGAAACGTCGTAATGAGA 327

QY 356 GAATTCATTTTCATGGGTGATCTTCAATGCTGCTGAGCTAGCTCCCAAGAGGCTG 415
Db 326 GAATTCATTTTCATGGGTGATCTTCAATGCTGCTGAGCTAGCTCCCAAGAGGCTG 267

QY 416 GAAGACATCCGCTGAGAGACGACCCCAAGTTGTTGGCTGATCGGGAGCCAAAGAGA 475
Db 266 GAAGACATCCGCTGAGAGACGACCCCAAGTTGTTGGCTGATCGGGAGCCAAAGAGA 207

QY 476 CACCACGTCAGAGAGACCAAACTGCGCTATGACAGATGCTGTTAGAGACAAAA 535
Db 206 CACCACGTCAGAGAGACCAAACTGCGCTATGACAGATGCTGTTAGAGACAAAA 147

QY 536 TATTGTCACTCTGTGGTCTCTCAATCAAACTGCTGTTGATTTCAGAAAGCTTACAG 595
Db 146 TATTGTCACTCTGTGGTCTCTCAATCAAACTGCTGTTGATTTCAGAAAGCTTACAG 87

QY 596 GTTGTCTGAATGAGAGCCCTGATGTCAGCGACCACTTTCAGTTCATCATCATCA 655
Db 86 GTTGTCTGAATGAGAGCCCTGATGTCAGCGACCACTTTCAGTTCATCATCATCA 27

RESULT 6
BE048177 666 bp mRNA linear EST 20-OCT-2000
LOCUS BE048177
DEFINITION t46b09.y1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2291681 5'
similar to SW:DHPP2_HUMAN Q13609 DNASE I HOMOLOGOUS PROTEIN DHP2
PRECUSOR ;, mRNA sequence.

ACCESSION BE048177
VERSION BE048177.1 GI:8365155
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 666)

REFERENCE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
TITLE (CGAP/BRAP), Tumor Gene Index

JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:

info@image.lnl.gov
Insert Length: 1048 Std Error: 0.00

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Seq primer: -40RP from Gibco
High quality sequence stop: 431.
Location/Qualifiers
1. .666
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/clone="IMAGE:2291681"
/clone_lib="NCI_CGAP_Brn52"
/lab_host="DH10B"
/lab_type="tumor, 5 pooled (see description)"
/Note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; This library represents the normalized
version of NCI CGAP_Brn35. Cloned unidirectionally.
Primer: Oligo dr. Average insert size 1.19 kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(grade II), medulloblastoma, astrocytoma (grade IV).
Constructed by Life Technologies."
BASE COUNT 198 a 149 c 170 g 147 t 2 others
ORIGIN

Query Match 68.3%; Score 458; DB 10; Length 666;
Best Local Similarity 88.1%; Pred. No. 8e-121;
Matches 497; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 1 ACAACAGGATCTGCCCATCTGATGGAAGCTAAACGGAATTCACAGAAAGGCATAA 60
Db 95 ACAACAGGATCTGCCCATCTGATGGAAGCTGACAGAAATTCACAGGAGGCATAA 154

QY 61 CATACAACTATGTGATTAGCTCTCGCCTTGGAGAAACACATATAAAGAACATATGCCT 120
Db 155 CGTACAACTATGTGATTAGCTCTCGCCTTGGAGAAACACATATAAAGAACATATGCCT 214

QY 121 TTCTCTATAAGAAAGCTAGTGTCTGTAAAAACAAAGCTACCTTACCACGACTATCAGG 180
Db 215 TTCTCTACAAGAAAGCTGGTGTCTGTGAAGAGAGTTATCACTACCATGACTATCAGG 274

QY 181 CTGGAGACGCAGATGTTTCCAGGAAACCCCTTGTGTCTGTGTTCCAGTCAACCCATCA 240
Db 275 ATGGAGACGCAGATGTTTCCAGGAGCCCTTGTGTCTGTGTTCCAAATCTCCCCACA 334

QY 241 CGCTGTCAAGGACTTCGTGATTGTCCCTCGCACACACCCCTCGAGCATCCGTTAGAG 300
Db 335 CTGCTGTCAAGACTTCGTGATTATCCCTCGCACACACCCCTCGAGCATCCGTTAGAG 394

QY 301 AGATTGAGCTGGCTGATGTCTACACAGATGTGAACCGTCTGGAATGCAGAGAAATT 360
Db 395 AGATCGATGAGTTGGTTGAGGTCTACACGAGCTGAACACCGCTGGAAGCGGAGAAATT 454

QY 361 TCATTTTCATGGTGACTTCATGCTGGCTGAGCTACGCTCCCAAGAGGCTCGAAGG 420
Db 455 TCATTTTCATGGTGACTTCATGCTGGCTGAGCTACGCTCCCAAGAGGCTCGAAGG 514

QY 421 ACATCCGCTGAGGAGCGGACCCAGTTCGTTGGCTGATCGGGACCAAGAGGACACA 480
Db 515 ACATCCGCTGAGGAGCTGACCCAGTTCGTTGGCTGATCGGGACCAAGAGGACACA 574

QY 481 CGGTCAAGAGAGCAACAACTCGCTCATGACAGGATCGTGTCTAGAGGACAAATATTG 540
Db 575 CGGTGAAGAGAGCAACCACTCGTGCATATGACAGGATTCGTTCTAGAGGACAAAGAAATC 634

QY 541 TCAACTCTGGTGGTCTCTCAATCAA 564
Db 635 GCAGTTCGTGTTCCTCCCAAGTCAA 658

RESULT 7
AW543356/c 642 bp mRNA linear EST 31-AUG-2000
LOCUS C0168H07-3 NIA Mouse E7.5 Extraembryonic Portion cDNA Library Mus
DEFINITION musculus cDNA clone C0168H07 3', mRNA sequence.
ACCESSION AW543356
VERSION AW543356.1 GI:7185773
KEYWORDS EST.
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SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 642)
AUTHORS Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H., III, Becker,K.G. and KO,M.S.H.
TITLE Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
MEDLINE 203811348
COMMENT Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6920, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0168 row: H column: 07
Seq primer: -21M13 Forward
High quality sequence stop: 642
POLYA=Yes.
Location/Qualifiers
1. .642
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:C0168H07-3"
/db_xref="taxon:10090"
/clone="C0168H07"
/clone_lib="NIA Mouse E7.5 Extraembryonic Portion cDNA Library"
/dev_stage="7.5dpc Embryo"
/lab_host="DH10B"
/Note="vector: pSPORT1 (Gibco/BRL Life Technology);
Site 1: Sali; Site 2: NotI; Total RNAs were extracted from
5 EPC. The double-stranded cDNA was synthesized by
Gibco's kit with an Oligo(dT) primer (NotI primer-adaptor
from GibcoBRL)
[5'-pGACTAGTTCAGTACGCGCGCCCTTTTTCCTTTTTCCTTTT-3']
from 0.8ug of mRNA. The double-stranded cDNAs were
treated with T4 DNA polymerase and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker LL-Sal3 (include Sali sequence). The cDNAs
were purified by phenol/chloroform and separated from
free linkers by Centricon 100. Then, cDNAs were amplified
by long-range high fidelity PCR using Takara's Ex Taq
polymerase. Then, the cDNAs were purified by
phenol/chloroform and by Centricon 100. The cDNAs were
digested with Sali and NotI enzymes. Then, the cDNAs were
size selected by Gibco's Size Fractionation Column. The
cDNAs were cloned into Sali/NotI site of pSPORT1 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by chemical method. The library was
constructed by Xiaohong Wang."
BASE COUNT 166 a 161 c 148 g 167 t
ORIGIN

Query Match 64.5%; Score 432.6; DB 10; Length 642;
Best Local Similarity 82.6%; Pred. No. 1.6e-113;
Matches 495; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 57 ATACATACAACTATGTGATTAGCTCTCGCCTTGGAGAAACACATATAAAGACGAT 116
Db 642 ACAATACAACTATGTGATTAGCTCTCGCCTTGGAGAAACACGTCACAGAGCAGTAT 583

QY 117 GCCTTTCTATAAGAAAGACTAGTGTCTGTAAAAACAAAGCTACCTTACACGACTAT 176
Db 582 GCCTTCGTCTACAAGGAGAAGCTGTGTCTGTGAAGACAAAATACCACTACCATGACTAT 523

QY 177 CAGGCTGGAGAGCAGATGTCTTTTCCAGGAAACCCCTTTTGGTCTGGTCCAGTCAACC 236
Db 522 CAGGATGGAGACACAGACGCTGTTCAGGAGGCCCTTTGTGGTTTGTTCATTCCCCC 463
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QY 237 TACCCGCTGTCAAGACCTTGTGATTTGTCCTCCCTGCAACCAACCCCTGAGACATCCGTT 296
 DB 462 TTTACTGCTGTCAAGACCTTGTGATTTGTCCTCCCTGCAACCAACCCCTGAGACATCCGTT 403
 QY 297 AGAGAGATGATGAGCTGGGTGATGTCCTACAGATGTGAAAAGTGTGGTGAATGAGAG 356
 DB 402 AAGAGATGATGAGCTGGGTGATGTCCTACAGATGTGAAAAGTGTGGTGAATGAGAG 343
 QY 357 AATTGATTTGATGAGGATCACTTCAATGCTGCTGACAGTACGTCCTCCCAAGAGGCTTG 416
 DB 342 AATTGATTTGATGAGGATCACTTCAATGCTGCTGACAGTACGTCCTCCCAAGAGGCTTG 283
 QY 417 AAGGATATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
 DB 282 CAGAAATTTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223
 QY 477 ACCACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
 DB 222 ACTACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 163
 QY 537 ATTGCACTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 596
 DB 162 ATAGTCACTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 103
 QY 597 TTGCTGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 655
 DB 102 TTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 44

RESULT 8
 B1522352/c 695 bp mRNA linear EST 29-AUG-2001
 LOCUS 60308142011 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220532 3'
 DEFINITION mRNA sequence.
 B1522352
 ACCESSION B1522352.1 GI:15347144
 VERSION EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 695)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LLM11554 row: h column: 05
 High quality sequence start: 18
 High quality sequence stop: 695.
 Location/Qualifiers
 1..695
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5220532"
 /clone_lib="NIH_MGC_120"
 /lab_host="DH10B"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb, insert size range 1-2.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 025. Note: this is a NIH_MGC Library."

FEATURES
 Source

BASE COUNT 159 a 171 c 163 g 202 t
 ORIGIN
 Query Match 63.9%; Score 428.8; DB 13; Length 695;
 Best Local Similarity 87.2%; Pred. No. 2.1e-112;
 Matches 516; Conservative 0; Mismatches 72; Indels 4; Gaps 4;
 QY 49 GAAAAGGATTAACATACATATGATTAAGTCTGCTGGAAGAAACATATAAG 108
 DB 695 GGAGAGCATTAACATACATATGATTAAGTCTGCTGGAAGAAACATATAAG 636
 QY 109 AACGATAGCTCTTCTCTATAAAGAAAGCTAGTCTGTAAACAACTACTAC 168
 DB 635 CACAAATATGCTCTTCTCTATAAAGAAAGCTAGTCTGTAAAGGATTAATCACTACC 576
 QY 169 ACAGCTATCAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 228
 DB 575 ATGACTATCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
 QY 229 AGTCAACCTTACA-CCGCTGTCAAGAGACTTGTGATTTGCCCTGACACACACCCCTGAG 287
 DB 515 AATCTCCCAATCTGCTGTCAAGAGACTTGTGATTTGCCCTGACACACACCCCTGAG 456
 QY 288 ACATCCGTTAAGAGATGATGAGTGGCT- GATGTCTACACAGATGTGAACCTGCTG 346
 DB 455 ACATCCGTTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 396
 QY 347 GAATCAGAGAAATTCATTTTCATGAGGAGCTTCAATGCTGCTGACGTAAGTCCCA 406
 DB 395 GAAGGCGAGAAATTCATTTTCATGAGGAGCTTCAATGCTGCTGACGTAAGTCCCA 336
 QY 407 GAAGGCTGGAAGAGATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 466
 DB 335 GAAGGCTGGAAGAGATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276
 QY 467 CCAAGAGAGACCAACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 526
 DB 275 CCAAGAGAGACCAACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 216
 QY 527 AGGCAAAATATTGTCATCTGAGTGTCTCAATCA-ACCTGCTTTGATTTCCAGA 585
 DB 215 AGGCAAAATATTGTCATCTGAGTGTCTCAATCA-ACCTGCTTTGATTTCCAGA 156
 QY 586 AAGCTTAAGGTTGTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 637
 DB 155 AAGCTTAAGGTTGTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 105

RESULT 9
 LOCUS BG687772 825 bp mRNA linear EST 29-MAY-2001
 DEFINITION 602786883F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4912893 5'
 mRNA sequence.
 BG687772
 ACCESSION BG687772.1 GI:14218312
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 825)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Db 566 TTGATTTTCATGGGTGACTTCAATCCGCGCTGCAGCTTACGTTCCAGAGAGGCTTGAAAC 625

QY 419 GGACATCCGCTGAGAGACGAGACCCCAAGTTGCTTTGGCTGATCGGGACCAAGAGACAC 478

Db 626 GAACATCCGCTGAGAGACGAGACCCCAAGTTGCTTTGGCTGATCGGGACCAAGAGACAC 685

QY 479 CACCGTCAAGAGACCAAACTGCGCCCTATGACAGGA-TGCTGCTTAAAGACAAAATA 537

Db 666 CACGCTGAAGAGACCAACTGTCATATGACAGATTGCTTACAGGACCAAGGA 745

QY 538 TTGTCACTCTGTGTGCTCTCAATCAATCAACCTGCTTTGATTTCCAGAAAGCTTACAGGT 597

Db 746 AATGCTCAAGTGTGTGCTCTCAAGTCAAGAGGCTTACTTCCAGAAAGCTTCCAGGC 805

QY 598 TGTCTGAATCGAAGGCTTG 617

Db 806 TGACTGTAGAAAGAGGCTTG 825

RESULT 11

LOCUS B1460950 628 bp mRNA linear EST 21-AUG-2001

DEFINITION 603207187P1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272917 5', mRNA sequence.

ACCESSION B1460950

VERSION B1460950.1 GI:15251606

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 628)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Plate: LLM11688 row: n column: 22
High quality sequence stop: 628.

FEATURES

source Location/Qualifiers

1..628

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5272917"

/clone_1lb="NIH_MGC_97"

/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gagcag) ; Oligo-CP primed using primer 5'-TTTTTTTCTTTTTCVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 181 a 144 c 166 g 137 t

ORIGIN

Query Match 61.9%; Score 415.4; DB 13; Length 628;
Best Local Similarity 90.6%; Pred. No. 1.5e-108;
Matches 443; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 ACAACAGATCTGCCCATCTAGTGAAGAACTAAACGAAATTCAGAAAGGCATTA 60

Db 140 ACAACAGATCTGCCCATCTAGTGAAGAACTAAACGAAATTCAGAAAGGCATTA 199

QY 61 CATACAAATATGTGATTAGCTCTGCGCTTGGAGAAACATATPAAGACATATGCTT 120

Db 200 CATACAACTATGATGATTAGCTCTGCGCTTGGAGAAACATATPAAGACATATGCTT 259

QY 121 TTCTCTATAAGAAAGTACTGTCGTAAACAAAGTACTCTTACACAGATATCAGG 180

Db 260 TTCTCTACAGAAAGTACTGTCGTAAAGAGAGATTATCATTACCATATATATCAGG 319

QY 181 CTGAGACGAGATGTTGTTTCCAGGAAACCTTTGTTGCTGTTGCTGCTGCTGCTGCT 240

Db 320 ATGAGACGAGATGTTGTTTCCAGGAGCCCTTTGTTGCTGTTGCTGCTGCTGCTGCT 379

QY 241 CCGCTGTAAAGACTTGTGATTTGCTCCCTGACACACCACCTTGAGACATCGTTAGAG 300

Db 380 CTGCTGTAAAGACTTGTGATTTATCCCTGACACACCACCTTGAGACATCGTTAGAG 439

QY 301 AGATTGATGAGCTGCTGATGCTTACACAGATGAAACGTCGCTGGAATGACAGAAAT 360

Db 440 AGATGATGAGCTGCTGATGCTTACACAGATGAAACGTCGCTGGAATGACAGAAAT 499

QY 361 TCATTTTCATGAGTACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Db 500 TCATTTTCATGAGTACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 559

QY 421 ACATCCGCTTGAAGACGAGACCCCAAGTTGCTTGGCTGATCGGGACCAAGAGACACCA 480

Db 560 ACATCCGCTTGAAGACGAGACCCCAAGTTGCTTGGCTGATCGGGACCAAGAGACACCA 619

QY 481 CGGTCAAGA 489

Db 620 CGGTCAAGA 628

RESULT 12

LOCUS AM543802/c 620 bp mRNA linear EST 31-AUG-2000

DEFINITION C0174C07-3 NIA Mouse E7.5 Extraembryonic Portion cDNA Library Mus

ACCESSION AM543802

VERSION AM543802.1 GI:7186219

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 620)

AUTHORS Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grabovac, M.J., Pantano, S., Sano, Y., Piao, Y., Negaraja, R., Doi, H., Wood, W.H., Ili, Becker, K.G. and Ko, W.S.H.

TITLE Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

MEDLINE 20381348

COMMENT Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: C0174 row: C column: 07
Seq primer: -21M13 Forward
High quality sequence stop: 620
PolyA+yes.

FEATURES

source Location/Qualifiers

1..620

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="nisl:EST:C0174C07-3"

/db_xref="taxon:10090"

/clone="C0174C07"

/clone_1lb="NIA Mouse E7.5 Extraembryonic Portion cDNA Library"

/sex="unknown"

/dev_stage="7.5dpc Embryo"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Gibco/BRL Life Technology);
Site 1: SalI; Site 2: NotI; Total RNAs were extracted from
5 EPC. The double-stranded cDNA was synthesized by
Gibco's kit with an oligo(dT) primer (NotI primer-adaptor
from GibcoBRL)
[5'-pGACTAGTCTAGATCGGAGCGGCCCTTTTTTTTTTTT-3']
from 0.8ug of mRNA. The double-stranded cDNAs were
treated with T4 DNA polymerase and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker LL-Sal3 (include SalI sequence). The cDNAs
were purified by phenol/chloroform and separated from
free linkers by Centricon 100. Then, cDNAs were amplified
by long-range high fidelity PCR using Takara's Ex Taq
polymerase. Then, the cDNAs were purified by
phenol/chloroform and by Centricon 100. The cDNAs were
digested with SalI and NotI enzymes. Then, the cDNAs were
size selected by Gibco's Size Fractionation Column. The
cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by chemical method. The library was
constructed by Xiaohong Wang."

BASE COUNT 160 a 159 c 143 g 158 t
ORIGIN
Query Match 61.4%; Score 412.2; DB 10; Length 620;
Best Local Similarity 82.1%; Pred. No. 1.2e-107;
Matches 474; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 79 GCTCTGCGCTTGGAGAAACACATATAAAGACAGTATCGCTTTCTCTATAAAGAAAGC 138
| | | | |
Db 620 GTTCTCGACTTGGAGAAACAGCTACAAAGACAGTATCGCTTTCGTCTAAGGAGAGC 561
| | | | |
QY 139 TAGTGTCTGTAAACAAAGCTACCTACACGACTATCAGCTCGAGCGCAGATGTCT 198
| | | | |
Db 560 TGGTGTCTGTGAAGCAAAATACCACTACCATGACTATCAGGATGGAGACAGACGCTGT 501
| | | | |
QY 199 TTTCCAGGGAACCTTTGTGGTCTGTGTTCCAGTCAACCTTACACCGCTGTCAAGGACTCG 258
| | | | |
Db 500 TTTCCAGGAGCCCTTTGGTTTGGTTCATCTCCCTTTACTGCTGTCAAGGACTCG 441
| | | | |
QY 259 TGATTTGTCCTTCGACACACCCCTTGAGACATCCGTTTAGAGAGATTGATGCTGGCTG 318
| | | | |
Db 440 TGATTTGTCCTTCGACACAACTCCGAGACCTCCGTTTAAAGAGATAGATGAGTGGTCG 381
| | | | |
QY 319 ATGCTCTACAGATGTGAACGTGCTGGAATGCAGAGAAATTCATTTTCATGGGTGACT 378
| | | | |
Db 380 ATGTCTACACGGATGTGAAGCCAGTGTGAAGACAGAGAAATTCATCTTTCATGGGTGATT 321
| | | | |
QY 379 TCAATGCTGGCTGCAGCTACGTCCCAAGAGCCCTGGAAGACATCCGCTTGAGGACGG 438
| | | | |
Db 320 TCAACGCCGCTGTAGTATGTCCCAAGAGCCCTGGCAGAACATTCGTTTGAAGACGG 261
| | | | |
QY 439 ACCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGACACACCGTCAAGAAAGACACAA 498
| | | | |
Db 260 ACCCAAGTTCGTTTGGCTGATTTGGGACCAAGAGACACTACGCTCAAGAAAGATACCA 201
| | | | |
QY 499 ACTGGCCTATACAGGATCGTCTTAGAGGACAAATATTGTCACATCTGTTGGTCTCTC 558
| | | | |
Db 200 GCTGTGCTATACAGGATGTGCTTTTGTGGACAGAGATAGTCAACTCCGTTGGTATCCCC 141
| | | | |
QY 559 AATCAACCTCGTCTTTGATTTCCAGAAAGCTTACAGGTTGTCTGAATCGAAGGCCCTGG 618
| | | | |
Db 140 GTTCAGTGGCGTCTTTGACTTTTCAAGAGCTTATGACTTTGTCTGAGGAGGAGGCCCTGG 81
| | | | |
QY 619 ATGTGAGCGACCACTTTCAGTTCATCATCATCA 655
| | | | |
Db 80 ATGTGAGTATCATCTTCCAGTTGAGTTTAAGCTACA 44
| | | | |

RESULT 13
AI927844/c

LOCUS AI927844 784 bp mRNA linear EST 08-MAR-2000
DEFINITION wo1909.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2462752 3',
similar to SW:DHP2.HUMAN Q13609 DNASE I HOMOLOGOUS PROTEIN DHP2
PRECUSOR ;, mRNA sequence.
ACCESSION AI927844
VERSION AI927844.1 GI:5663808
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 784)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 739 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 426.
Location/Qualifiers
1..784
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2462752"
/clone_lib="NCI CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
plasmid DNA from the normalized library NCI CGAP Kid1;
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 173 a 188 c 179 g 242 t 2 others
ORIGIN
Query Match 60.8%; Score 407.8; DB 9; Length 784;
Best Local Similarity 86.1%; Pred. No. 2.5e-106;
Matches 451; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 132 GAAAGCTAGTGTCTGTAAACAAAGCTACTCTACACGACTATCAGGCTGGAGACGCA 191
| | | | |
Db 667 GAAAGCTGGTGTCTGTGAAGAGGAGTATCACTACCATGACTATCAGATGGAGACGCA 608
| | | | |
QY 192 GATGTGTTTTCCAGGAAACCTTTGTGCTGTGTTCCAGTCAACCTACACGCTCTCAAG 251
| | | | |
Db 607 GATGTGTTTTCCAGGAGCCCTGTGTGCTGTGTTTCCAATCTCCCCACACTGCTGTCAA 548
| | | | |
QY 252 GACTTCGTGATTGTCCCTCTGCACACCACTCTGAGACATCGTTTAGAGAGATTGATGAG 311
| | | | |
Db 547 GACTTCGTGATTATCCCTCTGCACACCAACCCAGACATCGTTTAGAGAGATCGATGAG 488
| | | | |
QY 312 CTGGCTGATGTTACACAGATGTGAACGTCGCTGGAATGCAGAGAAATTTCAATTTTCATG 371
| | | | |
Db 487 TTGTTTGAAGTCTACACGACGTGAACACACCGCTGGAAGCGGAGAAATTTCAATTTTCATG 428
| | | | |
QY 372 GGTGACTTCAATGTGGCTGCAGCTACGTCCTCCCAAGAGGCTTGAAGGACATCCGCTG 431
| | | | |
Db 427 GGTGACTTCAATGTGGCTGCAGCTACGTCCTCCCAAGAGGCTTGAAGGACATCCGCTT 368
| | | | |

QY 432 AGGACGAGACCCCAAGTTCGTTGGCTGATCGGGAGACCAAGACCAACGCTCAGAAG 491
 DB 367 AGGACTGACCCCAAGTTCGTTGGCTGATCGGGAGACCAAGACCAACGCTCAGAAG 308
 QY 492 AACACAAATGCGCCCTATGACAGATCGTGTAGAGACAAATAATTGTCACTGTGT 551
 DB 307 AGCACCACATGTGACATATGACAGATGTGTAGAGACCAAGAAATGCTCACTGTGT 248
 QY 552 GGTCTCAATCAAACTGCTTTGATTTCCAGAAAGCTTACAGTGTGTGAATGAAG 611
 DB 247 GTTCCCAAGTCAAACTGCTTTGATTTCCAGAAAGCTTACAGTGTGTGAATGAAG 188
 QY 612 GCCCTGGATGTGACGACCACTTTCAGTTCATCATCATCA 655
 DB 187 GCCCTGGATGTGACGACCACTTTCAGTTCATCATCA 144

RESULT 14
 AM540389/c
 LOCUS AM540389 610 bp mRNA linear EST 31-AUG-2000
 DEFINITION C0132C04-3 NIA Mouse E7.5 Extraembryonic Portion cDNA Library Mus
 musculus cDNA clone C0132C04 3', mRNA sequence.
 ACCESSION AM540389
 VERSION AM540389.1 GI:7182806
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 610)
 Tanaka, T.S., Jardatz, S.A., Lim, M.K., Kargul, G.J., Mang, X., Granovac,
 M.J., Becker, K.G., and Ko, M.S.H.
 I11, Beck, K.G., and Ko, M.S.H.
 Genome-wide expression profiling of mid-gestation placenta and
 embryo using a 15,000 mouse developmental cDNA microarray
 Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
 20381348
 COMMENT Contact: George J. Kargul
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cda@igsun-grc.nia.nih.gov
 Plate: C0132 row: C column: 04
 Seq primer: -21M13 Forward
 High quality sequence stop: 610
 POLY(A)=yes.

FEATURES
 source
 location/Qualifiers
 1..610
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:C0132C04-3"
 /db_xref="taxon:10090"
 /clone="C0132C04"
 /clone_11b="NIA Mouse E7.5 Extraembryonic Portion cDNA
 library"
 /sex="unknown"
 /dev_stage="7.5dpc Embryo"
 /lab_host="DH10B"
 /note="vector: pSPORT1 (Gibco/BRL life technology);
 Site 1: SalI; Site 2: NotI; Total RNAs were extracted from
 5 EPC. The double-stranded cDNA was synthesized by
 Gibco's kit with an Oligo(dt) primer [NotI primer-adaptor
 from Gibco/BRL]
 [5'-pGACTAGTCTAGATCGGAGCGGCCCTTTTCTTTTCTTTT-3']
 from 0.8ug of mRNA. The double-stranded cDNAs were
 treated with T4 DNA polymerase and purified by
 ethanol-precipitation. The cDNAs were ligated to
 lone-linker l1-sal3 (include sal1 sequence). The cDNAs
 were purified by phenol/chloroform and separated from
 free linkers by Centricon 100. Then, cDNAs were amplified
 by long-range high fidelity PCR using Takara's Ex Taq
 polymerase. Then, the cDNAs were purified by
 phenol/chloroform and by Centricon 100. The cDNAs were

digested with SalI and NotI enzymes. Then, the cDNAs were
 size selected by Gibco's Size Fractionation Column. The
 cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid
 vector. The DH10B E. coli host was transformed with the
 ligation mixture by chemical method. The library was
 constructed by Xiaohong Wang."

BASE COUNT 157 a 157 c 140 g 156 t
 ORIGIN

Query Match 60.7%; Score 407; DB 10; Length 610;
 Best Local Similarity 82.4%; Pred. No. 3.8e-106;
 Matches 467; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 89 TGGAGAAACACATATTAAGAACTAGTCTTCTATTAAGAAAGCTAGTCTGT 148
 DB 610 TGGAGAAACACATATTAAGAACTAGTCTTCTATTAAGAAAGCTAGTCTGT 551
 QY 149 AAAACAAGCTACCTCTACCAAGCTATCAGGCTGAGAACGCAATGTGTTCCAGGA 208
 DB 550 GAAACAAGCTACCTCTACCAAGCTATCAGGCTGAGAACGCAATGTGTTCCAGGA 491
 QY 209 ACCCTTGTGTGTTGTTCCAGTACCTTACAGCGCTGTCAAGGACTGTGATGTCC 268
 DB 430 GCCCTTGTGTGTTGTTCCAGTACCTTACAGCGCTGTCAAGGACTGTGATGTCC 431
 QY 269 CCTGCACACACCCCTGAGACATCGTTAGAGATGATGAGTGTCTACAC 328
 DB 430 CTTGCACACACCTCCGAGACCTCGTTAAGAGATGATGAGTGTCTACAC 371
 QY 329 AGATGTAAGCTGCTGAGATGAGAGATTTTATTTTCTGATGCTTCAATGCTGG 388
 DB 370 GATGTGAGAGCTGAGATGAGAGATTTTATTTTCTGATGCTTCAATGCTGG 311
 QY 389 CTGACGCTACCTCCCAAGAGAGCTGAGAGATCGCTGAGAGAGAGAGAGAGAG 448
 DB 310 CTGACGCTACCTCCCAAGAGAGCTGAGAGATCGCTGAGAGAGAGAGAGAGAG 251
 QY 449 GCTTTGCTGATCGGAGACCAAGAGACCAAGAGATCGCTGAGAGAGAGAGAGAG 508
 DB 250 TGTTTGCTGATCGGAGACCAAGAGAGCTGAGAGATCGCTGAGAGAGAGAGAGAG 191
 QY 509 TGACAGATCGGCTGAGAGACCAAGATATGTAACCTGTGTCTCATCAAACT 568
 DB 190 TGACAGATCGGCTGAGAGACCAAGATATGTAACCTGTGTCTCATCAAACT 131
 QY 569 GCTTTGATTTCCAGAAAGCTTACAGGTTGTTGAATCGAAGGCCCTGTGATGACGA 628
 DB 130 GCTTTGATTTCCAGAAAGCTTACAGGTTGTTGAATCGAAGGCCCTGTGATGACGA 71
 QY 629 CCATTTCACTTATCATCATCA 655
 DB 70 TCATTTCACTTATCATCATCA 44

RESULT 15
 AM915564
 LOCUS AM915564 668 bp mRNA linear EST 25-MAY-2000
 DEFINITION EST346868 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
 RGCW80 5' end, mRNA sequence.
 ACCESSION AM915564
 VERSION AM915564.1 GI:8081263
 KEYWORDS EST.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 668)
 AUTHORS Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
 Kerlavage, A.R., and Adams, M.D.
 TITLE Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
 Gene Index
 JOURNAL Unpublished (1998)

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2002, 08:59:53 ; Search time 40.9082 Seconds
(without alignments)
5030.295 Million cell updates/sec

Title: US-09-905-114-3
Perfect score: 671
Sequence: 1 acaacagatctgccccata.....atcatcatgaagaaccatga 671

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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4: /cgn2_6/prodata/1/ina/6B-COMB.seq: *
5: /cgn2_6/prodata/1/ina/PCTUS-COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481.2	71.7	1208	1	US-08-640-765A-2
2	481.2	71.7	1208	3	US-09-073-613-2
3	163.2	24.3	1039	1	US-07-895-300A-2
4	163.2	24.3	1039	4	US-09-638-112-2
5	163.2	24.3	1039	5	PCT-US93-05136-2
6	163.2	24.3	1039	5	PCT-US93-10519-1
7	161.6	24.1	1039	1	US-08-458-367-2
8	124.6	18.6	1615	2	US-08-491-988-15
9	124.6	18.6	1624	2	US-08-491-988-14
10	124.6	18.6	1648	2	US-08-491-988-13
11	119	17.7	1055	2	US-08-468-012A-1
12	119	17.7	1055	4	US-09-054-989-1
13	35.2	5.2	1427	3	US-09-173-581-10
14	35.2	5.2	1427	4	US-08-420-915-10
15	32.8	4.9	1293	2	US-08-924-440-1
16	32.2	4.8	289	4	US-09-007-005-17
17	32.2	4.8	289	4	US-09-244-796-17
18	32.2	4.8	7218	1	US-08-232-463-14
19	31.8	4.7	1511	2	US-08-809-763-3
20	31.8	4.7	1511	3	US-08-956-253-3
21	31.6	4.7	1001	4	US-09-641-638-90
22	31.2	4.6	248	3	US-08-513-974B-300
23	31.2	4.6	248	3	US-08-513-974B-301
24	30.6	4.6	1920	1	US-08-487-753-1
25	30.6	4.6	1920	2	US-08-480-065-1
26	30.6	4.6	1920	3	US-08-487-744-1
27	30.6	4.6	1920	5	PCT-US93-09167-1

C 28	30.6	4.6	2900	2	US-09-027-337-9	Sequence 9, Appli
C 29	30.6	4.6	2900	4	US-09-644-600-9	Sequence 1, Appli
C 30	30.6	4.6	3147	2	US-09-027-337-1	Sequence 1, Appli
C 31	30.6	4.6	3147	4	US-09-644-600-1	Sequence 1, Appli
C 32	30.6	4.6	3147	4	US-09-644-600-18	Sequence 18, Appli
C 33	30	4.5	1734	4	US-09-484-970B-63	Sequence 63, Appli
C 34	30	4.5	2071	1	US-07-923-724-1	Sequence 1, Appli
C 35	30	4.5	2071	2	US-08-609-426A-1	Sequence 1, Appli
C 36	30	4.5	2071	2	US-08-374-652C-3	Sequence 3, Appli
C 37	30	4.5	4049	1	US-08-162-809-17	Sequence 17, Appli
C 38	30	4.5	4097	1	US-08-162-809-11	Sequence 11, Appli
C 39	29.8	4.4	3981	2	US-08-955-138-2	Sequence 2, Appli
C 40	29.6	4.4	47	4	US-09-146-054-7	Sequence 7, Appli
C 41	29.6	4.4	47	4	US-09-664-977A-7	Sequence 7, Appli
C 42	29.6	4.4	270	4	US-09-146-054-8	Sequence 8, Appli
C 43	29.6	4.4	270	4	US-09-664-977A-8	Sequence 8, Appli
C 44	29.6	4.4	352	4	US-09-228-986-21	Sequence 21, Appli
C 45	29.6	4.4	560	3	US-09-042-426-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-640-765A-2
; Sequence 2, Application US/08640765A
; Patent No. 5821103
; GENERAL INFORMATION:
; APPLICANT: Tanuma, Sei-ichi
; TITLE OF INVENTION: NOVEL DEOXYRIBONUCLEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,765A
; FILING DATE: 06-MAY-1996
; CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6239518
; FILING DATE: 06-SEP-1994
; CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
; NAME: Green, Robert F.
; REGISTRATION NUMBER: 27555
; REFERENCE/DOCKET NUMBER: 73362
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 12..941
US-08-640-765A-2

Query Match 71.7%; Score 481.2; DB 1;
Best Local Similarity 85.1%; Pred. NO. 5.8e-139;
Matches 550; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

QY 1 ACAACGAGTCTGCCCTACTGATGAGAGAGCTAAACGGAATTCAGAAAAAGCATTA 60
DB 217 ACAACAAACATCTGCTCCAGCTGATGAGAGAGCTGATGAGAACTCACAGAAAGACGA 276
QY 61 CATACAACTATGATTTAGCTCTGCGCTTGAGAGAAACATATTAAGAACATATGCT 120
DB 277 CATACAACTATGATTTAGCTCTGCGCTTGAGAGAAACATATTAAGAACATATGCT 336
QY 121 TTCTCTATTAAGAAAAAGTAGTGTCTGTAACAAAGCTACCTCTACACGATATCAG 180
DB 337 TCCTCTACAAAGAGAGAGCTGTGTCTGTAGAGCAAAAATACCTACATGACTATCAG 396
QY 181 CTGAGAGCGCAATGTGTCTTCCAGAGAACCTTTGTGTCTGTGTCTGTGTCTGTGT 240
DB 397 ATGAGAGACACAGCGTGTCTTCCAGAGAACCTTTGTGTGTGTGTGTGTGTGTGTGT 456
QY 241 CCGCTGTCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 457 CTGCTGCCAAGAGACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 516
QY 301 AGATTGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 517 AGATGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 576
QY 361 TCATTTCATGGGTGACTTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 577 TCATTTCATGGGTGACTTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 636
QY 421 ACATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 637 ACATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 696
QY 481 CGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 697 CGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 756
QY 541 TCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 757 TCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 816
QY 601 CTGAATCGAAGGCCCTG--GATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
DB 817 CTGAAGAGAGAGGCCCTGATGATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 862

RESULT 2
US-09-073-613-2
; Sequence 2, Application US/09073613
; Patent No. 6143875
; GENERAL INFORMATION:
; APPLICANT: Tanuma, Sei-ichi
; TITLE OF INVENTION: ANTIBODY TO NOVEL DEOXYRIBONUCLEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,613
; FILING DATE: 06-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/640,765
; FILING DATE:

APPLICATION NUMBER: JP 6239518
FILING DATE: 06-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: LARCHER, Carol
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 85519
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 12..941
US-09-073-613-2

Query Match 71.7%; Score 481.2; DB 3; Length 1208;
Best Local Similarity 85.1%; Pred. No. 5.8e-139;
Matches 550; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

QY 1 ACAACGAGTCTGCCCTACTGATGAGAGAGCTAAACGGAATTCAGAAAAAGCATTA 60
DB 217 ACAACAAACATCTGCTCCAGCTGATGAGAGAGCTGATGAGAACTCACAGAAAGACGA 276
QY 61 CATACAACTATGATTTAGCTCTGCGCTTGAGAGAAACATATTAAGAACATATGCT 120
DB 277 CATACAACTATGATTTAGCTCTGCGCTTGAGAGAAACATATTAAGAACATATGCT 336
QY 121 TTCTCTATTAAGAAAAAGTAGTGTCTGTAACAAAGCTACCTCTACACGATATCAG 180
DB 337 TCCTCTACAAAGAGAGAGCTGTGTCTGTAGAGCAAAAATACCTACATGACTATCAG 396
QY 181 CTGAGAGCGCAATGTGTCTTCCAGAGAACCTTTGTGTCTGTGTCTGTGTCTGTGT 240
DB 397 ATGAGAGACACAGCGTGTCTTCCAGAGAACCTTTGTGTGTGTGTGTGTGTGTGTGT 456
QY 241 CCGCTGTCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 457 CTGCTGCCAAGAGACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 516
QY 301 AGATTGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 517 AGATGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 576
QY 361 TCATTTCATGGGTGACTTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 577 TCATTTCATGGGTGACTTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 636
QY 421 ACATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 637 ACATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 696
QY 481 CGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 697 CGGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 756
QY 541 TCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 757 TCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 816
QY 601 CTGAATCGAAGGCCCTG--GATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
DB 817 CTGAAGAGAGAGGCCCTGATGATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 862

RESULT 3
US-07-895-300A-2
; Sequence 2, Application US/07895300A

Patent No. 5279823
GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/895,300A
FILING DATE: 19920608
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 747
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1039 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-895-300A-2

Query Match 24.3%; Score 163.2; DB 1; Length 1039;
Best Local Similarity 57.4%; Pred. No. 9.5e-41;
Matches 335; Conservative 0; Mismatches 243; Indels 6; Gaps 2;

QY 60 ACATACAATGATGATTAGCTCTCGCTTGGAGAACACATATATAAGAACAGTATGCC 119
DB 409 ACCTATCACTAGCTGCTAGTGAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTG 468
QY 120 TTCTCTATAAAGAAAGCTAGTGTCTGTAAACAAAGCTACCTTACCACGA---CTAT 176
DB 469 TTCTGTACAGGCTGACAGGTGTCTGGGTGGACAGTACTACTACGATGATGCTGC 528
QY 177 CAGGCTGGAGAGCAGATGTGTTTCCAGGGAACCCCTTTGTGGTCTGTTCCAGTACCCC 236
DB 529 GAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATGTCAGGTTCTTCTCCCGG 588
QY 237 TACACCGCTGTCAAGACTCTGATGATGTCCTCCCTGACACACCCCTGAGACATCCGTT 296
DB 589 TTCACAGAGTCAAGGAGTTTGCATGTTCCCTGATGCGGCGCCCGGGGACGAGTA 648
QY 297 AGAGAGATTGATGAGCTGGCTGATGTCTACAGATGTGAACGCTCGCTGGAATGCAGAG 356
DB 649 GCGGAGATCGAGCTCTTATGACGCTACCTGGATGTCACAGAGAAATGGGCTTGGAG 708
QY 357 AATTCAATTTTCATGGGTGACTTCAATGTGGCTGACGCTACGTCCTCCCAAGAGGCGCTGG 416
DB 709 GAGCTCATGTTGATGGGCACTTCAATGCGGCTGCGAGCTATGTGAGACCCCTCCCACTGG 768
QY 417 AAGGACATCGGCTGAGGAGGAGCCCAAGTTGTTGGCTGATCGGGGACCAAGAGGAC 476
DB 769 TCATCATCCGCTGTGGACAAGCCCACTTCCAGTGGCTGATCCCGCCAGACGCGCTGAC 828

QY 477 ACCAGGTCACAGAGAGACACAACTGCGCTATGACAGGATCGTCTTAGAGGACAAAAT 536
DB 829 ACCACAG---CTACACCCAGGCACTGTGCTATGACAGGATCGTGGTTGCAGGATGCTG 885
QY 537 ATTGCAACTCTGGTGGTCTCAATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGG 596
DB 886 CTCGAGGCGCGTGTGTTCCCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCTATGCG 945
QY 597 TTGTCGTAATCAAGGCGCTGATGTCAGGACCACTTTTCCAGT 640
DB 946 CTGAGTGACCAACTGCGCCCAAGCCATCAGTGACCACTATCCAGT 989

RESULT 4

US-09-638-112-2
Sequence 2, Application US/09638112
Patent No. 6440412
GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,112
FILING DATE: 09-Aug-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/942561
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: P0747C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3562
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1039 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-638-112-2

Query Match 24.3%; Score 163.2; DB 4; Length 1039;
Best Local Similarity 57.4%; Pred. No. 9.5e-41;
Matches 335; Conservative 0; Mismatches 243; Indels 6; Gaps 2;

QY 60 ACATACAATGATGATTAGCTCTCGCTTGGAGAACACATATATAAGAACAGTATGCC 119
DB 409 ACCTATCACTAGCTGCTAGTGAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTG 468
QY 120 TTCTCTATAAAGAAAGCTAGTGTCTGTAAACAAAGCTACCTTACCACGA---CTAT 176
DB 469 TTCTGTACAGGCTGACAGGTGTCTGGGTGGACAGTACTACTACGATGATGCTGC 528
QY 177 CAGGCTGGAGAGCAGATGTGTTTCCAGGGAACCCCTTTGGTCTGTTCCAGTACCCC 236
DB 529 GAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATGTCAGGTTCTTCTCCCGG 588

QY 237 TACACCGCTGTCAAGAGCTTGTGATGTCCTCCCTGACACACCCCTTGAGACATCCGTT 296
 Db 589 TTCAAGAGGTCAGAGAGATTGTCATGTTCCCTGACAGCGCCCGGGGAGCAGTA 648
 QY 237 AGAGATGATGAGCTGGCTGATGTCACAGATGTAAGAAAGTCGCGTAATGAGAG 356
 Db 649 GCCGAGATCGAGCTCTCTATGACGTCCTACCTGAGATGTCAGAGAAATGAGGCTTGGAG 708
 QY 357 AATTCATTTTCATGAGGTCATTCATGTCGAGTCAGCTAGCTCCCAAGAGGCTTGG 416
 Db 709 GACGTCATGTTGATGGGCACTTCATGAGGAGGCTGAGCTATGAGACCTCCAGTGG 768
 QY 417 AAGACATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
 Db 769 TCATCCATCCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 828
 QY 477 ACCACGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
 Db 829 ACCACAG---CTACACCCAGCAGCTGTGATGACAGAGATGTTGACAGGAGTCTG 885
 QY 537 ATTGTCAACTGTGTGTCCTCAATCAAACTGCTTTGATTTTCAGAAAGCTTACAG 596
 Db 886 CTCGAGGCGCGCTGTTCCGAGCTGCGCTTCCCTTTAATTCCAGGCTGCTATGAGC 945
 QY 597 TTGTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 640
 Db 946 CTGAGTGACCAACTGCGCCCAAGCAGATGAGACCACTATCCAGT 989

RESULT 5

PCT-US93-05136-2
 ; Sequence 2, Application PC/TUS9305136

; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; TITLE OF INVENTION: PURIFIED FORMS OF DNase
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/05136
 ; FILING DATE: 19930528
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Johnston, Sean A.
 ; REGISTRATION NUMBER: P35,910
 ; REFERENCE/DOCKET NUMBER: 747PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-3562
 ; TELEFAX: 415/952-9881
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1039 bases
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; PCT-US93-05136-2

Query March

24.3%, Score 163.2; DB 5; Length 1039;

Best Local Similarity 57.4%; Pred. No. 9.5e-41;
 Matches 335; Conservative 0; Mismatches 243; Indels 6; Gaps 2;

QY 60 ACATPACACTGTGATGATGCTCTGCTTGGAGAAACATATTAAGACAGTATGCC 119
 Db 409 ACCTATGCTAGTGTGATGAGCACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 468
 QY 120 TTTCTCTATAAAGAAAGCTAGTGTCTGTAAACAAAGCTTACCTTACACAG---CTAT 176
 Db 469 TTGCTGTCAGAGCCGTGACAGAGTGTCTGCGTACAGACTACTACTAGATGAGGCTGC 528
 QY 177 CAGGCTGAGAGAGAGATGTTTTCAGAGGAGACCTTTGAGTGTGCTGCTCACTCACCC 236
 Db 529 GAGCCCTCGGAAACGACACTTCAACCGAGAGCAGACATGTCAGAGTCTTCTCCCG 588
 QY 237 TACACCGCTGTCAAGAGCTTGTGATGTCCTCCCTGACACACCCCTGAGACATCCGTT 296
 Db 589 TTCAAGAGAGTCAGAGAGATTGTCATGTTCCCTGATGCGGCCCGGGGAGCAGTA 648
 QY 237 AGAGAGATTGATGAGCTGCTGATGTCACAGATGTAAGAGTGCCTGAGATGAGAG 356
 Db 649 GCCGAGATCGAGCTCTCTATGACGTACCTGATGTCAGAGAAATGAGGCTTGGAG 708
 QY 357 AATTCATTTTCATGAGGATGTCATGTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
 Db 709 GACGTCATGTTGATGGGAGCTTCAATGCGGCTGAGCTGATGTAAGACCTCCAGTGG 768
 QY 417 AAGACATCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
 Db 769 TCATCCATCCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 828
 QY 477 ACCACGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
 Db 829 ACCACAG---CTACACCCAGCAGCTGTGATGACAGAGATGTTGACAGGAGTCTG 885
 QY 537 ATTGTCAACTGTGTGTCCTCAATCAAACTGCTTTGATTTTCAGAAAGCTTACAG 596
 Db 886 CTCGAGGCGCGCTGTTCCGAGCTGCGCTTCCCTTTAATTCCAGGCTGCTATGAGC 945
 QY 597 TTGTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 640
 Db 946 CTGAGTGACCAACTGCGCCCAAGCAGATGAGACCACTATCCAGT 989

RESULT 6

PCT-US93-10519-1
 ; Sequence 1, Application PC/TUS9310519

; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; TITLE OF INVENTION: Compaction Assay for Assessment of Respiratory Disease
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/10519
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Johnston, Sean A.

Db 829 ACCACAG---CTACACCCAGCAGCTGTGCTTATGACGAGATGTGTCAGGAGTCGTG 885
Qy 537 ATTGTCAACTGTGTGTGCTTCATCAATCAAACTGCTTTGATTTCCAGAACTTACAGG 596
Db 886 CTCGACGCGCGCTGTGTTCCGACTCGGCTCTTCCCTTTAACTTCCAGGCTCCTATGCG 945
Qy 597 TTGTCTGAATCGAAGCCCTGTGATGTACGACCACTTTCCAGT 640
Db 946 CTGAGTGAACCACTGGCCCAAGCCATCAGTACCACTATCCAGT 989

RESULT 8

US-08-491-988-15
; Sequence 15, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMENON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCALULAY NISSEN GOLDBERG KIEL & HAND, LLP
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,988
; FILING DATE: 18-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDBERG, JULES E.
; REGISTRATION NUMBER: 24,408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-986-4090
; TELEFAX: 212-818-9479
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1615 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
US-08-491-988-15

Query Match 18.6%; Score 124.6; DB 2; Length 1615;
Best Local Similarity 53.2%; Pred. No. 1e-28;
Matches 312; Conservative 0; Mismatches 269; Indels 6; Gaps 2;
Qy 60 ACATACAACTATGTGATTAGCTCTGCTTGGAGAAACATATATAAGACATATGCC 119
Db 1009 ACCATCACTAGTGTGTTTTCGAAACCCCTCGGGCGTAACTTTACAAAGAACGTAAGT 1068
Qy 120 TTTCTCTATAAAGAAAGCTAGTGTCTGTAATAAACAAGCTACTTACACAGAC---TAT 176
Db 1069 TTCCTGTCCGTCGCAAAAGTTTCAGTACTGATACCTACAGTACGACGAGATGC 1128
Qy 177 CAGGCTGAGACGAGATGTGTTTCCAGGGAACCTTTGTGCTGTGGTTCAGTACACCC 236
Db 1129 GAATTTTCGCTAGACACTTTTCTCCGGGAACCGGCTGTGTTAAATTTTCGAGCCAC 1188
Qy 237 TACACCGCTGTCAAGACTTGTGTAATGTCCCCCTGCACACACCCCTGAGACATCCGTT 296
Db 1189 TCTACCAAGTTAAAGAGTTCGCTATGCTGTCTGACAGAGGCGCGTCTGAGCTGTT 1248

Qy 297 AGAGAGATTGATGAGCTGCTGATGTCTACACAGATGTGAACGCTCGGAATGCAGAG 356
Db 1249 GCTGAATCACTCTCTGTACGAGGTTTACCTGGACGTTGAGAAATGGCACCTGAC 1308
Qy 357 AATTTCATTTTCATGGGTGATTTCAATGCTGGCTGCAGCTACGTTCCCAAGAGCGCTGG 416
Db 1309 GACGTCAGCTGAATGGGGGATTTCAACGCTGACCTCTTATATGATACCTTCTCAGTGG 1368
Qy 417 AAGGACATCCGCTGAGAGACGCAACCCAGTTGCTTTGGCTGATCGGAGACCAAGAGAC 476
Db 1369 TCATGATTCGCTGCGCAGCTCTGCACTTCCAGTGCTGATCCGAGCTCCGCTGAC 1428
Qy 477 ACCACGCTCAAGAAAGACACAACTGCGCTATGACAGATGCTGTAGAGACAAAT 536
Db 1429 ACCACGCTACT--AGTACCACTGCGCTTACAGACCGTATGTTGTGCTGATCCCTG 1485
Qy 537 ATTGTCAACTGTGTGTGCTTCATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGG 596
Db 1486 CTGAGTCTTCTGTGTAACCGGTAAGCGCGCCCGTTGCACTTCAGGCTGCATATGCT 1545
Qy 597 TTGTCTGAATCGAAGCCCTGTGATGTACGACCACTTTCCAGTTCA 643
Db 1546 CTTTCGAACGAATGGCGCTGCGCATCTGTGATCACTACCGGTTGA 1592

RESULT 9

US-08-491-988-14
; Sequence 14, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMENON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCALULAY NISSEN GOLDBERG KIEL & HAND, LLP
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,988
; FILING DATE: 18-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDBERG, JULES E.
; REGISTRATION NUMBER: 24,408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-986-4090
; TELEFAX: 212-818-9479
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
US-08-491-988-14

Query Match 18.6%; Score 124.6; DB 2; Length 1624;
Best Local Similarity 53.2%; Pred. No. 1e-28;
Matches 312; Conservative 0; Mismatches 269; Indels 6; Gaps 2;
Qy 60 ACATACAACTATGTGATTAGCTCTGCGCTTGGAAAGAAACATATATAAGACATATGCC 119

Db 1018 ACCTACACCTACCTGTTTCTGTAACCCCTCGGCGTAACCTTTACAAAGAACGGTACCTG 1077
QY 120 TTTCTCTATAAAGAAAGCTAGTGTCTGTAAAAACAAGCTACCTCTACCAAGAC---TAT 176
Db 1078 TTTCTGTTCCGTCGGAACAAAGTTTCAGTACTGGATACCTACAGTACGACGACGATGC 1137
QY 177 CAGGCTGGAGACGAGATGTTTTCAGGGAACCTTTGTGTGTCTGTGTTTCCAGTACACC 236
Db 1138 GAATCTTGGCGTAACGACTCTTTCTCCGGAACCGGCTGTGTTAAATTTCTCGAGCCAC 1197
QY 237 TACACCGCTGTCAAGACTTCGTAATGTTCCCTCGACACCAACCCCTGAGACATCCGTT 296
Db 1198 TCTACCAAGTTAAAGATTTCGCTATGCTGTCTGCACACGCGCGCTGTGACGCTGTT 1257
QY 297 AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAAGCTCGCTGGAATCGAGAG 356
Db 1258 GCTGGAATCAACTCTCTGTACGAGGTTTACCTGGAGCTTCAGCAGAAATGGCACCTGAAC 1317
QY 357 AATTTCAATTTCAAGGAGCTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 416
Db 1318 GAGCTCATGTGATGCTGACTTCAACGCTGACTGCTCTTATGTAACCTCTTCTCAGTGG 1377
QY 417 AAGGACATCCGCTGAGGACGACCCCAAGTTCTGTTTGGCTGATCGGGACCAAGAGGAC 476
Db 1378 TCATCGATTGCTGTGCGCACTCGTGCACCTTCCAGTGGCTGATCCCGGACTCCGCTGAC 1437
QY 477 ACCACCGTCAAGAAGAGCACAAACTCGGCTATGACAGGATCGTGTGTAGAGGACAAAT 536
Db 1438 ACCACCGCTACT---AGTACCAACTGCGCTTACGACCGTATGCTGTGTGTGTGTGTGTGT 1494
QY 537 ATTGTCAACTCTGGTGTCTCTCAATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGG 596
Db 1495 CTGCACTCTTCTGTACCGGTAGCGGCGCCGCTGACCTTCCAGGCTGCATATGTT 1554
QY 597 TTGCTGTAATCGAGCCCTGATGTACGGACCACTTTTCCAGTTCA 643
Db 1555 CTTTTCGAACGAATGCGCTGGCCATCTCTGATCACTACCCCGTTGA 1601

RESULT 10

US-08-491-988-13

; Sequence 13, Application US/08491988

; Patent No. 5973116

; GENERAL INFORMATION:

; APPLICANT: EPENETOS, AGAMENNON A.

; APPLICANT: SPOONER, ROBERT A.

; APPLICANT: DEONARAIN, MAHENDRA

; TITLE OF INVENTION: Compounds for targeting

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP

; STREET: 261 MADISON AVENUE

; CITY: NEW YORK

; STATE: NY

; COUNTRY: USA

; ZIP: 10016-2391

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/491,988

; FILING DATE: 18-DEC-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: GOLDBERG, JULES E.

; REGISTRATION NUMBER: 24,408

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-986-4090

; TELEFAX: 212-818-9479

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1648 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; US-08-491-988-13

Query Match 18.6%; Score 124.6; DB 2; Length 1648;

Best Local Similarity 53.2%; Pred. No. 1e-28; Indels 6; Gaps 2;

Matches 312; Conservative 0; Mismatches 269; Indels 6; Gaps 2;

QY 60 ACATACAACATATGTGATTAGCTCTCGCCCTTGAAGAAACACATATAAAGAACAGTATGCC 119

Db 1042 ACCTACCACTACGTTGTTCTTGAACCCCTCGGCGTAACTCTTACAAAGAACGGTACTCG 1101

QY 120 TTTCTCTATAAAGAAAGCTAGTGTCTGTAAAAACAAGCTACCTCTACCAAGAC---TAT 176

Db 1102 TTCTCTGTTCCGTCGGAACAAAGTTTTCAGTACTGGATACCTACCAAGTACGACGACGATGC 1161

QY 177 CAGGCTGGAGACGAGATGTGTTTCCAGGGAACCCCTTGTGTGTGTGTGTGTGTGTGTGTGT 236

Db 1162 GAATCTTGGCGTAAAGCTCTTCTCCCGGAACCGGCTGTTGTTAAATTTCTGAGCCAC 1221

QY 237 TACACCGCTGTCAAGGACTTTCGTGATTGTTCCCTCGCACACCAACCCCTGAGACATCCGTT 296

Db 1222 TCTACCAAGTTAAAGAGTTCCGTATCGTTGCTCTGCACAGCGCGCGCTCTGACGCTGTT 1281

QY 297 AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTCGTCGTCGTCGTCGTCG 356

Db 1282 GCTGAAATCAACTCTCTGTACGACGTTTACCTGGAGCTTCAGCAGAAATGGCACCTGAAC 1341

QY 357 AATTTCAATTTTCATGGTGACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 416

Db 1342 GACGTCATGCTGATGGTGACTTCAACGCTGACTGCTTATGTATTAACCTCTTCTCAGTGG 1401

QY 417 AAGGACATCCGCTCGAGGACGACCCCAAGTTTCGTTTGGCTGATCGGGACCAAGAGGAC 476

Db 1402 TCATCGATTCTGCTCGGCACCTCGTCGACCTTCCAGTGGCTGATCCCGGACTCCGCTGAC 1461

QY 477 ACCAGGTCAGAAGAGACACAACTGGCGCTATGACAGGATCGTGTGTAGAGGACAAAAT 536

Db 1462 ACCACCGCTACT---AGTACCAACTGCGCTTACGACCGCTATCGTTGTTGCTGGATCCCTG 1518

QY 537 ATTGTCAACTCTGGTGTCTCTCAATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGG 596

Db 1519 CTGCAAGTCTTCTGTTGTACCGGCTAGCGCGCCCGCTTCCAGGCTGCATATGTT 1578

QY 597 TTGTCTGAATCGAAGCCCTCGATGTGACGACCACTTTTCCAGTTCA 643

Db 1579 CTTTTCGAACGAATGCGCTGCGCATCTCTGATCACTACCCCGTTGA 1625

RESULT 11

US-08-468-012A-1

; Sequence 1, Application US/08468012A

; Patent No. 5810744

; GENERAL INFORMATION:

; APPLICANT: RUBEN, ET AL.

; TITLE OF INVENTION: Human DNase

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,012A
 FILING DATE: 6 JUNE 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04954
 FILING DATE: 5 MAY 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 325800-428
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1055 BASE PAIRS
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: CDNA
 US-08-468-012A-1

Query Match: 17.7%; Score 119; DB 2; Length 1055;
 Best Local Similarity 55.4%; Pred. No. 4.3e-27;
 Matches 252; Conservative 1; Mismatches 196; Indels 6; Gaps 1;

Db 186 GACGAGATGTTTTCAGGAGACCTTGTGCTGTTCCAGTCAACCCACACCGCT 245
 359 GAGGATGACGTTTGGCCGGAGCCATTGTGGCCCACTTTCTTTGGCCAGCATGTC 418
 Qy 246 GTCAAGACTTCGTATGTTCCCTGCAACACACCCCTGAGACATCCGTTAGAGATT 305
 Db 419 CTTCACACCTGCTGTGTGTCCTGCGTGCACACACCTCTTAAGCCGTAGAGAGAGCTG 478
 Qy 306 GATGAGCTGCTGATGTCTACACAGATGTGAACGTCGTGAAATGACAGATTTCATT 365
 Db 479 AACGCCCTCTAGATGTGTCTGTGAGGTCTCCAGCACTGGCAAGAGACGTCGATC 538
 Qy 366 TTCAATGAGTGAATTCATATGCTGCTGACAGCTACGTCCTCAAGAAAGCCCTGAAAGACATC 425
 Db 539 CTGCTTGGGAGCTTCAATGCTGACTGCGCTTACTGACCAAAAAGCCCTGAGCAAGCTG 598
 Qy 426 CGCCTGAGAGAGACCCCAAGTTGTTGGCTGATCGGGAGCAAGAGACACACGCTC 485
 Db 599 GSGCTGCGAGTGAACCGAGCTTCCACTGGGTGATGCGGATGGGAGAGACACCAAGTG 658
 Qy 486 AAGAAGACACAAATGGCCCTATAGACAGATCGTGTCTTAAGAGACAAATATTGTCAAC 545
 Db 659 CGGGCAGACCCCACTGATATACCGCGTGTGCTGACAGGGGA-----GGCTGC 712
 Qy 546 TCTGTGTGCTCAATCAAACTGCTTTGATTTCCAGAAAGCTTACAGTTGTCTGAA 605
 Db 713 CGGAGTCTGCTGACACTGCGGCTGCTTGACTTCCCAAGAGCTTCCAGTCAAGAG 772
 Qy 606 TCGAAGGCTTGATGTACGACGACCACTTTCCAGT 640
 Db 773 GAGGAGGCCCTCAACATCAGTACACCACTAACCCGT 807

RESULT 12
 US-09-054-989-1
 Sequence 1, Application US/09054989
 Patent No. 6251648
 GENERAL INFORMATION:
 APPLICANT: RUBEN, ET AL.
 TITLE OF INVENTION: Human DNase
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH DISKETTE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/054,989
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/468,012
 FILING DATE: 6-JUNE-1995
 APPLICATION NUMBER: PCT/US94/04954
 FILING DATE: 5 MAY 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 325800-428
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1055 BASE PAIRS
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: CDNA
 US-09-054-989-1

Query Match: 17.7%; Score 119; DB 4; Length 1055;
 Best Local Similarity 55.4%; Pred. No. 4.3e-27;
 Matches 252; Conservative 1; Mismatches 196; Indels 6; Gaps 1;

Qy 186 GACGAGATGTTTTCAGGAGACCTTGTGCTGTTCCAGTCAACCCACACCGCT 245
 359 GAGGATGACGTTTGGCCGGAGCCATTGTGGCCCACTTTCTTTGGCCAGCATGTC 418
 Db 246 GTCAAGACTTCGTATGTTCCCTGCAACACACCCCTGAGACATCCGTTAGAGATT 305
 Qy 419 CTTCACACCTGCTGTGTGTCCTGCGTGCACACACCTCTTAAGCCGTAGAGAGAGCTG 478
 Db 246 GTCAAGACTTCGTATGTTCCCTGCAACACACCCCTGAGACATCCGTTAGAGATT 305
 Qy 419 CTTCACACCTGCTGTGTGTCCTGCGTGCACACACCTCTTAAGCCGTAGAGAGAGCTG 478
 Db 306 GATGAGCTGCTGATGTCTACACAGATGTGAACGTCGTGAAATGACAGATTTCATT 365
 Qy 479 AACGCCCTCTAGATGTGTCTGTGAGGTCTCCAGCACTGGCAAGAGACGTCGATC 538
 Db 306 GATGAGCTGCTGATGTCTACACAGATGTGAACGTCGTGAAATGACAGATTTCATT 365
 Qy 479 AACGCCCTCTAGATGTGTCTGTGAGGTCTCCAGCACTGGCAAGAGAGAGCTGATC 538
 Qy 366 TTCAATGAGTGAATTCATATGCTGCTGACAGCTACGTCCTCAAGAAAGCCCTGAAAGACATC 425
 Db 539 CTGCTTGGGAGCTTCAATGCTGACTGCGCTTACTGACCAAAAAGCCCTGAGCAAGCTG 598
 Qy 426 CGCCTGAGAGAGACCCCAAGTTGTTGGCTGATCGGGAGCAAGAGACACACGCTC 485
 Db 599 GSGCTGCGAGTGAACCGAGCTTCCACTGGGTGATGCGGATGGGAGAGACACCAAGTG 658
 Qy 486 AAGAAGACACAACTGGCCCTATAGACAGATCGTGTCTTAAGAGACAAATATTGTCAAC 545
 Db 659 CGGGCAGACCCCACTGATATACCGCGTGTGCTGACAGGGGA-----GGCTGC 712
 Qy 546 TCTGTGTGCTCAATCAAACTGCTTTGATTTCCAGAAAGCTTACAGTTGTCTGAA 605
 Db 713 CGGAGTCTGCTGACACTGCGGCTGCTTGACTTCCCAAGAGCTTCCAGTCAAGAG 772
 Qy 606 TCGAAGGCTTGATGTACGACGACCACTTTCCAGT 640
 Db 773 GAGGAGGCCCTCAACATCAGTACACCACTAACCCGT 807

RESULT 13

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US-09-173-581-10
; Sequence 10, Application US/09173581A
; Patent No. 6013455
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/173,581A
; CURRENT FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 119819
US-09-173-581-10

Query Match      5.2%; Score 35.2; DB 3; Length 1427;
Best Local Similarity 53.7%; Pred. No. 0.39;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 348 AATGCAGAGAATTTTCATTTTCATGGTGACTTCAATGCTGGTGCAGCTACGTCGCCCAAG 407
DB 857 AATGCAGATAAGATCAAGATCAGACCTCGGCAACGCTGCTGGGTGCACAAG 916
QY 408 AAGCCTCGAAGAGACATCCGCTGAGAGCGGACCCCAAGTTCGTTTGGCTGATCGGGGAC 467
DB 917 CACTTCACGGAAGACATCCAGACTCGGCAAGTACCGGCGCTCGAGTGTGATCGGGGCC 976
QY 468 CAAGAGGACACCAACGG 483
DB 977 GAATACGGCCCCCGG 992

RESULT 14
US-09-420-915-10
; Sequence 10, Application US/09420915
; Patent No. 6264947
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/420,915
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/173,581
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 119819
US-09-420-915-10

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Query Match      5.2%; Score 35.2; DB 4; Length 1427;
Best Local Similarity 53.7%; Pred. No. 0.39;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 348 AATGCAGAGAATTTTCATTTTCATGGTGACTTCAATGCTGGTGCAGCTACGTCGCCCAAG 407
DB 857 AATGCAGATAAGATCAAGATCAGACCTCGGCAACGCTGCTGGGTGCACAAG 916
QY 408 AAGCCTCGAAGAGACATCCGCTGAGAGCGGACCCCAAGTTCGTTTGGCTGATCGGGGAC 467
DB 917 CACTTCACGGAAGACATCCAGACTCGGCAAGTACCGGCGCTCGAGTGTGATCGGGGCC 976
QY 468 CAAGAGGACACCAACGG 483
DB 977 GAATACGGCCCCCGG 992

RESULT 15
US-08-924-440-1
; Sequence 1, Application US/08924440
; Patent No. 5871550
; GENERAL INFORMATION:
; APPLICANT: Frits et al.
; TITLE OF INVENTION: MUTANT THERMONOSPOA SPP. CELLULOSE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,440
; FILING DATE: August 27, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Christopher L. Stone
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GC388
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 846-7555
; TELEFAX: (650) 845-6504
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-924-440-1

Query Match      4.9%; Score 32.8; DB 2; Length 1293;
Best Local Similarity 58.0%; Pred. No. 2.1;
Matches 58; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 377 CTTCAATGCTGCTGCTAGCTCCCAAGAAGCGCTGGAAGGACATCCGCTGAGGAC 436
DB 1080 CTACACCGGTGACGGCGCAACGACTTCAGATGGCCGCCCTACATCGACTGATGTC 1139
QY 437 GGACCCCAAGTTCGTTTGGCTGATCGGGGACCAAGAGGAC 476
DB 1140 GGAACGGAAGATCGGGTGGACCAAGTGGAACTACTCTCGGAC 1179

Search completed: December 9, 2002, 09:19:58

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Mon Dec 9 13:45:04 2002

Job time : 57.9082 secs

us-09-905-114-3.rni

Page 10

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2002, 09:00:58 ; Search time 133.35 Seconds
(without alignments)
1962.092 Million cell updates/sec

Title: US-09-905-114-3
Perfect score: 671
Sequence: 1 acaacagatctgccccata.....atcatcatgaagaaccatga 671

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Gapop 10_0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues
Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/ECT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/ECTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	671	100.0	671	10	US-09-905-114-3
2	592	88.2	592	10	US-09-905-114-1
3	527	78.5	1023	10	US-09-962-436-336
4	527	78.5	1023	10	US-09-954-456-271
5	527	78.5	1023	10	US-09-880-107-3392
6	527	78.5	1079	12	US-10-133-085-1
7	527	78.5	1079	12	US-10-074-509-1
8	474.8	70.8	1124	12	US-10-133-065-11
9	474.8	70.8	1124	12	US-10-074-509-11
c 10	195.6	29.2	392	10	US-09-880-107-630
11	163.2	24.3	1039	10	US-09-771-078-1
12	163.2	24.3	1039	10	US-09-825-012-2
13	161.6	24.1	783	10	US-09-825-012-4
14	161.6	24.1	858	10	US-09-825-012-6
15	161.6	24.1	1548	10	US-09-825-012-62
16	161.6	24.1	1548	10	US-09-825-012-63
17	161.6	24.1	1548	10	US-09-825-012-65
18	161.6	24.1	1554	10	US-09-825-012-34
19	161.6	24.1	1554	10	US-09-825-012-35

20	161.6	24.1	1554	10	US-09-825-012-37	Sequence 37, Appl
21	161.6	24.1	1557	10	US-09-825-012-64	Sequence 64, Appl
22	161.6	24.1	1560	10	US-09-825-012-72	Sequence 72, Appl
23	161.6	24.1	1560	10	US-09-825-012-73	Sequence 73, Appl
24	161.6	24.1	1560	10	US-09-825-012-75	Sequence 75, Appl
25	161.6	24.1	1560	10	US-09-825-012-77	Sequence 77, Appl
26	161.6	24.1	1560	10	US-09-825-012-78	Sequence 78, Appl
27	161.6	24.1	1560	10	US-09-825-012-79	Sequence 79, Appl
28	161.6	24.1	1563	10	US-09-825-012-36	Sequence 36, Appl
29	161.6	24.1	1566	10	US-09-825-012-67	Sequence 67, Appl
30	161.6	24.1	1566	10	US-09-825-012-68	Sequence 68, Appl
31	161.6	24.1	1566	10	US-09-825-012-70	Sequence 70, Appl
32	161.6	24.1	1569	10	US-09-825-012-74	Sequence 74, Appl
33	161.6	24.1	1575	10	US-09-825-012-69	Sequence 69, Appl
34	161.6	24.1	1578	10	US-09-825-012-81	Sequence 81, Appl
35	161.6	24.1	1578	10	US-09-825-012-82	Sequence 82, Appl
36	161.6	24.1	1578	10	US-09-825-012-84	Sequence 84, Appl
37	161.6	24.1	1584	10	US-09-825-012-39	Sequence 39, Appl
38	161.6	24.1	1584	10	US-09-825-012-40	Sequence 40, Appl
39	161.6	24.1	1584	10	US-09-825-012-42	Sequence 42, Appl
40	161.6	24.1	1587	10	US-09-825-012-83	Sequence 83, Appl
41	161.6	24.1	1590	10	US-09-825-012-91	Sequence 91, Appl
42	161.6	24.1	1590	10	US-09-825-012-92	Sequence 92, Appl
43	161.6	24.1	1590	10	US-09-825-012-94	Sequence 94, Appl
44	161.6	24.1	1593	10	US-09-825-012-41	Sequence 41, Appl
45	161.6	24.1	1596	10	US-09-825-012-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-09-905-114-3
; Sequence 3, Application US/09905114
; Patent No. US20020048745A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, HUANNIN
; APPLICANT: AX, ROY L
; APPLICANT: BELLIN, MARY E
; TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDE SEQUENCES ENCODING A FERTILITY ASSOCIATED
; FILE REFERENCE: 21070US20
; CURRENT APPLICATION NUMBER: US/09/905,114
; PRIOR FILING DATE: 2001-07-14
; PRIOR APPLICATION NUMBER: US 60/218,140
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Bos sp.
US-09-905-114-3

Query Match	100.0%	Score 671;	DB 10;	Length 671;
Best Local Similarity	100.0%;	Pred. No. 1.4e-205;		
Matches 671;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	ACAAAGGATCTGCCCATCTGATGGAGAACTAAACGGAATTCAGAAAGGCATAA	60		
Db 1	ACAAAGGATCTGCCCATCTGATGGAGAACTAAACGGAATTCAGAAAGGCATAA	60		
Qy 61	CATACAACTATGTGATTAGCTCTCGCCTTGGAGAAACACATATAAAGACAGTATGCCT	120		
Db 61	CATACAACTATGTGATTAGCTCTCGCCTTGGAGAAACACATATAAAGACAGTATGCCT	120		
Qy 121	TTCTCTATAAAGAAAGCTAGTGTCTGTAAACAAAGCTACCTTACCAGCTATCAGG	180		
Db 121	TTCTCTATAAAGAAAGCTAGTGTCTGTAAACAAAGCTACCTTACCAGCTATCAGG	180		
Qy 181	CTTGAGACCCAGATGTTTTCCAGGAAACCCCTTTGTGGTCTGGTTCAGTACCCCTACA	240		
Db 181	CTTGAGACCCAGATGTTTTCCAGGAAACCCCTTTGTGGTCTGGTTCAGTACCCCTACA	240		

QY 241 CCGCTGTGAAGACTTCTGATGTTGCCCCCTGCACACCACCCCCTGAGATCCCTTAGAG 300
DB 241 CCGGTGTCAAGACTTCTGATGTTGCCCCCTGCACACCACCCCCTGAGATCCCTTAGAG 300
QY 301 AGATTGATGAGCTGGCTGATGCTCTACACAGATGTGAAACGTGCTGAAATGAGAAATT 360
DB 301 AGATTGATGAGCTGGCTGATGCTCTACACAGATGTGAAACGTGCTGAAATGAGAAATT 360
QY 361 TCATTTTCATGGGTGACTTCAATGCTGCTGAGCTACGCTCCCAAGAAAGCTTGAAGG 420
DB 361 TCATTTTCATGGGTGACTTCAATGCTGCTGAGCTACGCTCCCAAGAAAGCTTGAAGG 420
QY 421 ACATCCGCTGAGAGCGAGACCCCAAGTTCGTTGGCTGATGGGGAGCCCAAGAGACACCA 480
DB 421 ACATCCGCTGAGAGCGAGACCCCAAGTTCGTTGGCTGATGGGGAGCCCAAGAGACACCA 480
QY 481 CCGTCAAGAGAGACCAAACTGCGCTTATGACAGATGCTGTTAGAGACAAATATTG 540
DB 481 CCGTCAAGAGAGACCAAACTGCGCTTATGACAGATGCTGTTAGAGACAAATATTG 540
QY 541 TCAACTCTGTGTGCTCTCAATCAAACTGCTTGTGATTTCCAGAAAGCTTACAGTTGT 600
DB 541 TCAACTCTGTGTGCTCTCAATCAAACTGCTTGTGATTTCCAGAAAGCTTACAGTTGT 600
QY 601 CTGAATCGAAGGCCCTGATGTGACGGACCACTTCCAGTTCAATCATCATCATCATG 660
DB 601 CTGAATCGAAGGCCCTGATGTGACGGACCACTTCCAGTTCAATCATCATCATCATG 660
QY 661 AAGAACCATGA 671
DB 661 AAGAACCATGA 671

RESULT 2
US-09-905-114-1

; Sequence 1, Application US/09905114
; Patent No. US20020048745A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, HUAMIN
; APPLICANT: AX, ROY L
; APPLICANT: BELLIN, MARY E
; TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDE SEQUENCES ENCODING A FERTILITY ASSOCIATED
; FILE REFERENCE: 210707US20
; CURRENT APPLICATION NUMBER: US/09/905,114
; PRIOR FILING DATE: 2001-07-14
; PRIOR APPLICATION NUMBER: US 60/218,140
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Bos sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION:
US-09-905-114-1

Query Match 88.2%; Score 592; DB 10; Length 592;
Best Local Similarity 100.0%; Pred. No. 3,1e-180;
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 GAGAAGCTAAACGAAATTCAGAAAGCATTAACATCAACTATGTATTAGCTCTGCG 86
DB 1 GAGAAGCTAAACGAAATTCAGAAAGCATTAACATCAACTATGTATTAGCTCTGCG 60
QY 87 CTGGAAGAAACATATTAAGAACAGATGCTTCTCTATTAAGAAAGCTAGTGTCT 146
DB 61 CTGGAAGAAACATATTAAGAACAGATGCTTCTCTATTAAGAAAGCTAGTGTCT 120
QY 147 GTAAACAAAGCTACCTTACACGACTATCAGGCTGAGAGCGAGATGTGTTTCCAGG 206

DB 121 GTAAACAAAGCTACCTTACACGACTATCAGGCTGAGAGCGAGATGTGTTTCCAGG 180
QY 207 GAACCCCTTTGTGTGTGTTGCTCACTACACCTTACACCGCTGTCAAGACCTTGTGATGTC 266
DB 181 GAACCCCTTTGTGTGTGTTGCTCACTACACCTTACACCGCTGTCAAGACCTTGTGATGTC 240
QY 267 CCCCTGCACACCCCTCTGAGACATCCGTTAGAGATTTAGAGCTGCTGATGTCTAC 326
DB 241 CCCCTGCACACCCCTCTGAGACATCCGTTAGAGATTTAGAGCTGCTGATGTCTAC 300
QY 327 ACAGATGAAACCTGCTGAGATGACAGAAATTTCAATTTTCAATGAGTCAATGCT 386
DB 301 ACAGATGAAACCTGCTGAGATGACAGAAATTTCAATTTTCAATGAGTCAATGCT 360
QY 387 GCGTGCAGCTACGTTCCCAAGAGGCTTGAAGAGACATCCGCTGAGAGCGAGACCCCAAG 446
DB 361 GCGTGCAGCTACGTTCCCAAGAGGCTTGAAGAGACATCCGCTGAGAGCGAGACCCCAAG 420
QY 447 TTGCTTTGCTGATCGGGGACCAAGAGACACACGCTCAAGAAAGACCAAACTGCGCC 506
DB 421 TTGCTTTGCTGATCGGGGACCAAGAGACACACGCTCAAGAAAGACCAAACTGCGCC 480
QY 507 TATGACAGATCGTCTTAGAGACAAATATTTGTCACCTGCTGAGTCTCAATCAAC 566
DB 481 TATGACAGATCGTCTTAGAGACAAATATTTGTCACCTGCTGAGTCTCAATCAAC 540
QY 567 CTGCTTTGATTTCCAGAAAGCTTACAGTGTGCTGAATGAAAGGCCCTGG 618
DB 541 CTGCTTTGATTTCCAGAAAGCTTACAGTGTGCTGAATGAAAGGCCCTGG 592

RESULT 3
US-09-962-436-336

; Sequence 336, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 336
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-336

Query Match 78.5%; Score 527; DB 10; Length 1023;
Best Local Similarity 87.8%; Pred. No. 3,4e-159;
Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1 ACAACAGATCTGCCCATCTGATGAGAGAGCTTAACGGAATTCAGAAAGGCACTAA 60
DB 215 ACAACAGATCTGCCCATCTGATGAGAGAGCTTAACGGAATTCAGAAAGGCACTAA 274
QY 61 CATCAACTATGTATTAGCTCTGCTTGGAGAGAAACATATTAAGAAACAGATGCTCT 120
DB 275 CGTACAACTATGTATTAGCTCTGCTTGGAGAGAAACATATTAAGAAACAGATGCTCT 334
QY 121 TTCTCTATAAGAAAGCTAGTGTCTGTAAACAAAGCTACTTACACGACTATCAGG 180
DB 335 TTCTCTATAAGAAAGCTAGTGTCTGTAAAGAGAGTTCATCACTACATGACTATCAGG 394
QY 181 CTGAGAGCGAGATGTGTTTCCAGGAGACCTTGTGATGCTGTTCCAGTCAACCTTCA 240
DB 395 ATGAGAGCGAGATGTGTTTCCAGGAGACCTTGTGATGCTGTTCCAGTCAACCTTCA 454

Best Local Similarity 87.8%; Pred. No. 3.4e-159;
Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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D 275 CGTACAACTATGTGATTTGCTCTGCGCTTTGGAAAGAACATATTAAGACGTATGCTT 334
QY 121 TTCCTATAAAGAAAGTAGTGTCTGTAAACAAAGCTACCTTACCAAGCACTATCAG 180
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D 395 ATGGAGAGCAGATGTGTTTTCAGAGAAACCTTTTGTGCTGTGTTCCAGTACCTTACA 454
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D 455 CTGCTGTCAAGGACTTGTGATTTGCTCCCTGCAACACCCCTGAGACATCCGTTAAG 514
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D 515 AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTGCTGAGATGAGAAATT 574
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QY 421 ACATCCGCTGAGAGCGAGACCCCAAGTTCGTTGGCTGATCGGGAGCAAGAGGACACCA 480
D 635 ACATCCGCTGAGAGCGAGACCCCAAGTTCGTTGGCTGATCGGGAGCAAGAGGACACCA 694
QY 481 CGGTCAAGAGAGCAACAACCTGCTTACAGAGATCGTGTGAGAGACAAATATTTG 540
D 695 CGGTCAAGAGAGCAACAACCTGCTTACAGAGATCGTGTGAGAGACAAATATTTG 754
QY 541 TCAACTCTGTGTGTCCTCAATCAAACTTCGTTGATTTCCAGAAAGCTTACAGATTGT 600
D 755 TCAACTCTGTGTGTCCTCAATCAAACTTCGTTGATTTCCAGAAAGCTTACAGATTGT 814
QY 601 CTGAATCGAAGGCGCTGATGTCAAGGACCACTTTCAGTTATCATCATCATCA 655
D 815 CTGAATCGAAGGCGCTGATGTCAAGGACCACTTTCAGTTATCATCATCATCA 869
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RESULT 6
US-10-133-065-1
Sequence 1, Application US/10133065
Patent No. US20020123122A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

TITLE OF INVENTION: HUMAN DNASE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/133,065

FILING DATE: 26-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/643,520

FILING DATE: 22/08/2000

APPLICATION NUMBER: 08/794827

FILING DATE: 04-Feb-1997

APPLICATION NUMBER: 60/109796

FILING DATE: 05-Feb-1996

ATTORNEY/AGENT INFORMATION:

NAME: Evans, David W

REGISTRATION NUMBER: C.F.R. 10.9(b)

REFERENCE/DOCKET NUMBER: P1000R1C3

TELEPHONE: 650/225-1739

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1079 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-133-065-1

Query Match

Best Local Similarity 78.5%; Score 527; DB 12; Length 1079;

Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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QY 1 ACAACAGGATCTGCCCACTAGTAGAGAACTTAAAGCAATTCAGAAAGGCATTA 60
D 261 ACAACAGGATCTGCCCACTAGTAGAGAACTTAAAGCAATTCAGAAAGGCATTA 320
QY 61 CATACACTATGTGATTTGCTCTGCGCTTTGGAAAGAACATATTAAGACGTATGCTT 120
D 321 CGTACAACTATGTGATTTGCTCTGCGCTTTGGAAAGAACATATTAAGACGTATGCTT 380
QY 121 TTCCTATAAAGAAAGTAGTGTCTGTAAACAAAGCTACCTTACCAAGCACTATCAG 180
D 381 TTCCTATAAAGAAAGTAGTGTCTGTAAACAAAGCTACCTTACCAAGCACTATCAG 440
QY 181 CTGAGAGCAGATGTGTTTTCAGAGAAACCTTTGTGCTGATTCAGACCTTACA 240
D 441 ATGGAGAGCAGATGTGTTTTCAGAGAAACCTTTGTGCTGATTCAGACCTTACA 500
QY 241 CCGCTGTCAAGGACTTGTGATTTGCTCCCTGCAACACCCCTGAGACATCCGTTAAG 300
D 501 CTGCTGTCAAGGACTTGTGATTTGCTCCCTGCAACACCCCTGAGACATCCGTTAAG 560
QY 301 AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTGCTGAGATGAGAAATT 360
D 561 AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTGCTGAGATGAGAAATT 620
QY 361 TCATTTTCATGGGTGACTTCAATGCTGCTGAGCTACGCTCCCAAGAGGCTTGAAG 420
D 621 TCATTTTCATGGGTGACTTCAATGCTGCTGAGCTACGCTCCCAAGAGGCTTGAAG 680
QY 421 ACATCCGCTGAGAGCGAGACCCCAAGTTCGTTGGCTGATCGGGAGCAAGAGACACA 480
D 681 ACATCCGCTGAGAGCGAGACCCCAAGTTCGTTGGCTGATCGGGAGCAAGAGACACA 740
QY 481 CCGTCAAGAGAGCAACAACCTGCTTACAGAGATCGTGTGAGAGACAAATATTTG 540
D 741 CCGTCAAGAGAGCAACAACCTGCTTACAGAGATCGTGTGAGAGACAAATATTTG 800
QY 541 TCAACTCTGTGTGTCCTCAATCAAACTTCGTTGATTTCCAGAAAGCTTACAGATTGT 600
D 801 TCAACTCTGTGTGTCCTCAATCAAACTTCGTTGATTTCCAGAAAGCTTACAGATTGT 860
QY 601 CTGAATCGAAGGCGCTGATGTCAAGGACCACTTTCAGTTATCATCATCATCA 655
D 861 CTGAATCGAAGGCGCTGATGTCAAGGACCACTTTCAGTTATCATCATCATCA 915
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RESULT 7

US-10-074-509-1
; Sequence 1, Application US/10074509
; Patent No. US20020142437A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; Baron, Will F.
; TITLE OF INVENTION: HUMAN DNASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/074,509
; FILING DATE: 11-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/643,520
; FILING DATE: 22/08/2000
; APPLICATION NUMBER: 08/794827
; FILING DATE: 04-Feb-1997
; APPLICATION NUMBER: 60/109796
; FILING DATE: 05-Feb-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnston, Sean A.
; REGISTRATION NUMBER: 35,910
; REFERENCE/DOCKET NUMBER: P1000R1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3562
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1079 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-074-509-1
Query Match 78.5%; Score 527; DB 12; Length 1079;
Best Local Similarity 87.8%; Pred. No. 3.5e-159;
Matches 575; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 1 ACAACAGGATCTGCCCATCTACTGATGGAAGCTAAACCGGAATTCACAGAAAAGGCATAA 60
DB 261 ACAACAGGATCTGCCCATCTACTGATGGAAGCTAAACCGGAATTCACAGAAAAGGCATAA 320
QY 61 CATACAACTATGTGATTAGCTCTCGCTTGGGAAGAACACATATAAAGAACAGTAGTGCCCT 120
DB 321 CGTACAACTATGTGATTAGCTCTCGCTTGGGAAGAACACATATAAAGAACATATGCTCT 380
QY 121 TTCTCTATAAGAAAAGCTAGTGTCTGTAAAAACAAAGCTACCTTACACGACTATCAGG 180
DB 381 TTCTCTACAGGAAAAGCTGGTGTCTGTGACAGAGGAGTTATCACTACCATGACTATCAGG 440
QY 181 CTGGAGACGCAGATGTTTTCCAGGAAACCCCTTTGTGTCTGGTTCCAGTCAACCTTACA 240
DB 441 ATGGAGACGCAGATGTTTTCCAGGAGCCCTTTGTGTCTGGTTCCAATCTCCCCACA 500
QY 241 CGCTGTCAAGGACTTCGTGATTGTTCCTCCCTGCACACACCCCTCGAGACATCCGTTAGG 300
DB 501 CTGCTGTCAAGACTTCGTGATTATCCCTCTGCACACACCCAGAGCATCCGTTAAGG 560
QY 301 AGATTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGCTGCGTGAATGCAGAGAATT 360

DB 561 AGATCGATGAGTTGGTTGAGTCTACACGGACGTGAAACACCGCTGGAAGGCGAGAATT 620
QY 361 TCATTTTCATGGGTGACTTCAATGCTGGCTGAGCTACGTCCTCCAGAGAGGCTCGAAGS 420
DB 621 TCATTTTCATGGGTGACTTCAATGCTGGCTGAGCTACGTCCTCCAGAGAGGCTCGAAGA 680
QY 421 ACATCCGCTGAGGACGACCCCAAGTTCTGTTGGCTGATCGGGGACCAAGAGGACACCA 480
DB 681 ACATCCGCTGAGGACGACCCCAAGTTCTGTTGGCTGATCGGGGACCAAGAGGACACCA 740
QY 481 CGTCAAGAAAGACCAAACTCGGCTTATGACAGGATCTGCTTAGAGGACAAAATATTG 540
DB 741 CGGTGAAGAAAGACCAAACTCGGCTTATGACAGGATCTGCTTAGAGGACAAAATCG 800
QY 541 TCAACTCTGCTGCTCTCAATCAAACTCTGTTGATTTCAGAAAGCTTACAGCTTGT 600
DB 801 TCAGTTCTGTTGTTCCCAAGTCAACAGTGTGTTTTCAGTTCAGAAAGCTTACAGCTGA 860
QY 601 CTGAATCGAAGGCCCTTGGATGTCAGCGACCACTTTCCAGTTTCATCATCATCATCA 655
DB 861 CTGAAGAGGAGGCCCTTGGATGTCAGCGACCACTTTCCAGTTTCATCATCATCATCA 915

RESULT 8

US-10-133-065-11
; Sequence 11, Application US/10133065
; Patent No. US20020123122A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; Baron, Will F.
; TITLE OF INVENTION: HUMAN DNASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/133,065
; FILING DATE: 26-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/643,520
; FILING DATE: 22/08/2000
; APPLICATION NUMBER: 08/794827
; FILING DATE: 04-Feb-1997
; APPLICATION NUMBER: 60/109796
; FILING DATE: 05-Feb-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: *See attached Limited Recognition under 37
; C.F.R. 10.9(b)
; REFERENCE/DOCKET NUMBER: P1000R1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1124 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-133-065-11

Query Match 70.8%; Score 474.8; DB 12; Length 1124;
Best Local Similarity 82.9%; Pred. No. 2,1e-142;
Matches 542; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

2 CAACGAGATCGCCCATCTGATGAGAGGTAACGGAATTCAGAAAAGGCTATAC 61
379 CAACACATCTGTCCCATCTGATGAGAGGTAACGGAATTCAGAAAAGGCTATAC 438
62 ATACACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 121
439 ATACACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 498
122 TCTCTATTAAGAAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 181
499 GGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 558
182 TGGAGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 241
559 TGGAGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
242 CGCTGTCAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
619 TGCTGTCAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 678
302 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
679 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738
362 CATTTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 421
739 CATTTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 798
422 CATCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 481
799 CATCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 858
482 GGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 541
859 GGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 918
542 CAACGAGATCGCCCATCTGATGAGAGGTAACGGAATTCAGAAAAGGCTATAC 601
919 CAACGAGATCGCCCATCTGATGAGAGGTAACGGAATTCAGAAAAGGCTATAC 978
602 TGAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 655
979 TGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1032

RESULT 9
US-10-074-509-11
Sequence 11, Application US/10074509
Patent No. US20020142437A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
Beaton, Will F.
TITLE OF INVENTION: HUMAN DNASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/074,509
FILING DATE: 11-Feb-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/643,520
FILING DATE: 22/08/2000
APPLICATION NUMBER: 08/794827
FILING DATE: 04-Feb-1997
APPLICATION NUMBER: 60/109796
FILING DATE: 05-Feb-1996
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: P100OR1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3562
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1124 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-074-509-11

Query Match 70.8%; Score 474.8; DB 12; Length 1124;
Best Local Similarity 82.9%; Pred. No. 2,1e-142;
Matches 542; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

2 CAACGAGATCGCCCATCTGATGAGAGGTAACGGAATTCAGAAAAGGCTATAC 61
379 CAACACATCTGTCCCATCTGATGAGAGGTAACGGAATTCAGAAAAGGCTATAC 438
62 ATACACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 121
439 ATACACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 498
122 TCTCTATTAAGAAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 181
499 GGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 558
182 TGGAGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 241
559 TGGAGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
242 CGCTGTCAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
619 TGCTGTCAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 678
302 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
679 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738
362 CATTTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 421
739 CATTTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 798
422 CATCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 481
799 CATCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 858
482 GGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 541
859 GGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 918
542 CAACGAGATCGCCCATCTGATGAGAGGTAACGGAATTCAGAAAAGGCTATAC 601
919 CAACGAGATCGCCCATCTGATGAGAGGTAACGGAATTCAGAAAAGGCTATAC 978
602 TGAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 655
979 TGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1032

RESULT 10

US-09-880-107-630/c
; Sequence 630, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 630
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA279676
US-09-880-107-630

Query Match 29.2%; Score 195.6; DB 10; Length 392;
Best Local Similarity: 84.9%; Pred. No. 5.4e-53;
Matches 219; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 398 CGTCCCAAGAAGCGCTGGAAGACATCCGCTTGAGGACGGACCCCAAGTTCGTTGGCT 457
Db 392 CGTCCCAAGAAGCGCTGGAAGACATCCGCTTGAGGACTGACCCCAAGTTCGTTGGCT 333
QY 458 GATCGGGGACCAAGAGACACACCGTCAAGAGAGACACAACTGCGCCCTATGACAGGAT 517
Db 332 GATCGGGGACCAAGAGAGACACACCGTCAAGAGAGACACCAACTGTGCATATGACAGGAT 273
QY 518 CGTGCTTAGAGGACAAATATCTCAACTCTGGTGTCTCAATCAAACTCGTCTTTGA 577
Db 272 TGTGCTTAGAGGACAAATATCTCAACTCTGGTGTCTCAATCAAACTCGTCTTTGA 213
QY 578 TTTCAGAAAGCTTACAGGTGTCTGAATCGAAGGCGCTGGATGTGAGGACCACTTTCC 637
Db 212 TTTCAGAAAGCTTACAGGTGTCTGAATCGAAGGCGCTGGATGTGAGGACCACTTTCC 153
QY 638 AGTTCATCATCATCA 655
Db 152 AGTTGAATTTAACTACA 135

RESULT 11

US-09-771-078-1
; Sequence 1, Application US/09771078
; Patent No. US20020034727A1
; GENERAL INFORMATION:
; APPLICANT: Mtsny, Randall J.,
; APPLICANT: Daugherty, Ann L.,
; APPLICANT: Patapoff, Thomas W.
; TITLE OF INVENTION: DNase Compaction Assay
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/771,078
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/971,019
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: 792
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3177
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1039 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-771-078-1

Query Match 24.3%; Score 163.2; DB 10; Length 1039;
Best Local Similarity 57.4%; Pred. No. 2.7e-42;
Matches 335; Conservative 0; Mismatches 243; Indels 6; Gaps 2;
QY 60 ACATACAACATATGTGATTAGCTCTCGCCTTGGAGAAACACATATATAAGACAGTATGCC 119
Db 409 ACCTATCATCTAGCTGTGCTAGTGAGCCACTGGGACGGAACAGCTATATAAGGAGCGCTACCTG 468
QY 120 TTTCTCTATAAAAGAAAGCTAGTGTCTGTAAAAACAAAGCTACCTCTACCAACGA---CTAT 176
Db 469 TTCTGTACAGCGCTGACAGGTGTCTGGGTGGACAGTACTACTACGATGATGCTGC 528
QY 177 CAGGCTGGAGACGAGATGTGTTTCCAGGGAACCTTTTGGTCTGGTTCAGTCACTC 236
Db 529 GAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATTGTTCAGGTTCTTCTCCCGG 588
QY 237 TACACCGCTGTCAAGGACTTCGTGATTGTCCCTTCACACACCCCTGAGACATCGGT 296
Db 589 TTACAGAGGTGAGGAGTTCGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAG 648
QY 297 AGAGAGATGATGAGCTGCTGATGTCTACACAGATGTGAAACGTCGCTGGAATGCAGAG 356
Db 649 GCGGAGATCGAGCTCTCTATGACGCTACCTGGATGTCCAGAGAAATGGGCTTGGAG 708
QY 357 AATTTCAATTTTCATGGGTGACTTCAATGTGCTGCTGAGTACGTCCTCCCAAGAGCGCTGG 416
Db 709 GAGTCAATGTTGATGGGACTTCAATGCGGCTGCAGCTATGTGAGACCTCCAGTGG 768
QY 417 AAGGACATCGGCTGAGGACGACCCCAAGTTGTTGGCTGATCGGGGACCAAGAGGAC 476
Db 769 TCATCCATCCGCTGTGGACAGCCCACTTTCCAGTGGCTGATCCCGACAGCGCTGAC 828
QY 477 ACCACGTCGAAGAAGAGACAAACTGCGCTATGACAGGATGCTGCTTAGAGAGCAAAAT 536
Db 829 ACACAG---CTACACCCACGACTGTGCTTATGACAGGATCGTGGTTGACGGATGCTG 885
QY 537 ATTTGCAACTCTGGTGGTCTCAATCAAACTCGTCTTTGATTTCCAGAAAGCTTACAGG 596
Db 886 CTCGAGGCGGCTTTGTTCCCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGC 945
QY 597 TTGTCGAATCGAAGCCCTGGATGTACGCGACCACTTTCCAGT 640
Db 946 CTGAGTGACCAACTGGCCCAAGCCACTAGTGACCACTATCCAGT 989

RESULT 12

US-09-825-012-2
; Sequence 2, Application US/09825012
; Patent No. US20020122798A1

```

; GENERAL INFORMATION:
; APPLICANT : Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO: 2
; LENGTH: 1039
; TYPE: DNA
; ORGANISM: Homo sapiens
us-09-825-012-2

Query Match      24.3%; Score 163.2; DB 10; Length 1039;
Best Local Similarity 57.4%; Pred.No. 2;7e-42;
Matches 335; Conservative 0; Mismatches 243; Indels 6; Gaps 2

Oy   60 ACATCAACATTATGTGATTCCTCGCCTTGGAGAAACACATATPAAAAACAGTATGCC 119
Db   409 ACCTTACTACTAGTGTCAGTAGAGCACCTGGACGGAACAAGCTATAAGAGCGCTACCTG 468
Oy   120 TTTCTCTATAAAGAAAAGCTAGTGTCTGTAAAACAAAGTACTCTTACCACGA--CTAT 176
Db   469 TTCGTGTACAGCCCTGCACCCAGGTGTCTGCGTGGACAGCTACTACTACATCATGATGCTGC 528
Oy   177 CAGGCTGGAGAGCAGATGTGTTTTCCAGGAAACCCCTTGTGTCGTGTTCCAGTACCCC 236
Db   529 GAGCCCTCGGGAGACGACACTTCAACGAGAACCCAGCATTGTCAAGTTCTTCTCCGG 588
Oy   237 TACACCGCTGTCAAGGACTTCTGTATGTTCCTCCCTGCACACCAACCCCTGAGACATCCGTT 296
Db   589 TTACACGAGAGTCAGGAGATTGGCATTTGTTCCCTTCATGCGGCCCCGGGGAGCCAGTA 648
Oy   297 AGAGAGTTGATGAGCTGGCTGATGTCTACACAGATGTGAAACGTGCTGGAAATGCAGAG 356
Db   649 GCCGAGATCGACGCTCTTATGACCTGACCTGGATGTCCAAGAAATGGGGCTTGGAG 708
Oy   357 AATTTCATTTTCATGGGTGACTTCAATGCTGGCTGACGTAAGTCCCCAAGAAGCGCTGG 416
Db   709 GACGTCATGTTGATGGGCGCACTTCAATGGGGCTGCAGCTATGTAGAACCTCCAGTGG 768
Oy   417 AAGGACATCCGCTTGAGAGCGSAGCCCAAGTTGCTTTGGCTGATGGGGAGCCAAAGAGAC 476
Db   769 TCATCATTCCTCGCTCTGTGGACAAGCCCCACCTTCCAGTGGCTGATCCCCACAGCCCTGAC 828
Oy   477 ACCACGGTCAAGAAAGACAACAACTGCGCTCTGACAGAGATGTGCTTATAGAGAACAAAT 536
Db   829 ACCAAG---CTACACCCACGACCTGTGCTTATGACAGAGATGTGTGGTTCAGAGGATGCTG 885
Oy   537 ATTGTCAACTGTGTGTGTCCTCAATCAAACTGTCTTTGATTTCCAGAAAGCTTACAGG 596
Db   886 CTCGAGGCGCGGTGTGTTCCGACATCGGCTTCTCCCTTTAATTCCAGGCTGCTATGGC 945
Oy   597 TTGTCTGAATCAAGAGCCCTGTGATGTCAAGGACCACTTTCAGT 640
Db   946 CTGAGTGAACCAACTGGCCCAAGCCATCTAGTACCACTATCCAGT 989

RESULT 13
US-09-825-012-4
; Sequence 4, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT : Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03

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      / PRIOR APPLICATION NUMBER: US 60/237,159
      / PRIOR FILING DATE: 2000-10-02
      / PRIOR APPLICATION NUMBER: GB 0008049.9
      / PRIOR FILING DATE: 2000-04-03
      / NUMBER OF SEQ ID NOS: 102
      / SOFTWARE: PatentIn version 3.1
      / SEQ ID NO 4
      / LENGTH: 783
      / TYPE: DNA
      / ORGANISM: Homo sapiens
US-09-825-012-4

Query Match          24.1%; Score 161.6; DB 10; Length 783;
Best Local Similarity 57.2%; Pred. No. 7.2e-42;
Matches 334; Conservative 0; Mismatches 244; Indels 6; Gaps 2;

OY   60 ACATCACTATGTGATTAGCTCTCGCCTTGGAAACACATATATAAAGAACAGTATGCC 119
DB   184 ACCATATCATAGTGTTGATGAGGACACTGTGGAGCGAACACTATTAAGAAGCGCTTACC 243
OY   120 TTTCCTCTAATAAGAAAAGCTAGTGTCTGTATAAACAAGACTACTCTATCACAG---CTAT 176
DB   244 TTCGTGTACAGGCCCTGCACAGGTGTCTCCGGTGGACAGCTACTACTAGATGATGGCTGC 303
OY   177 CAGGCTGAGAGACGACGATGTGTTTTCCAGGAACCCCTTGTGTGTGGTTCCAGTCACCC 236
DB   304 GAGCCCTCGGGGAACGACACCTTCAACCGAAGAGCAGCCACTTGTACAGGTTCTTCCCGG 363
OY   237 TACACCGCTGTCAAAGGACTTGTTGATTTGTCCCCTGCACACACCCCTGAGACATCCGTT 296
DB   364 TTCACAGAGTGTCAGGAGATTGTTCCATTGTTCCCTGTGCATGCGCCCCGGGGAGCGAGTA 423
OY   297 AGAGAGATTGATGAGCTGCTGATGTCTPACAAGATGTGAACGTCGCTGAGATGACAGAG 356
DB   424 GCCGAGATCGACGCTCTATGACGTCTACTGATGTCCAAGAAATGGGGCTTGGAG 483
OY   357 AATTTCATTTTCATGGGTGACTTCAATGTCGTGGCTGACCTACGTCCCAAGAAGCCTGG 416
DB   484 GACGTCATTTGATGAGGGGACTTCAATGCGGGCTGCAGCTATGTGAGACCTCCACATGG 543
OY   417 AAGGACATCCGCTGAGAGCCGAGCCCAAGTTCGTTGGCTGATGCGGGACCAAGAGAGAC 476
DB   544 TCATCATTCGCGCTGTGGACAAGCCCACTTCCAGTGGCTGATGCCGACAGCGCTGAC 603
OY   477 ACCAGCGTCAAGAAAGACACAAATCGCGCTTATGACAGAGATGTGCTTAGAGACAAAT 536
DB   604 ACCACAG---CTACACCCACGACCTGTGCTTATGACAGGATCGTGGTTCAGGATGCTG 660
OY   537 ATTGCACTCTGGTGTGCTTCATTCAAACCTGCTTGTGATTTCCAGAAAGCTTACAGG 596
DB   661 CTCGAGGGGGCGCTTTGTTCCGACTCGGCTTTCCCTTTAACTTCCAGGCTGCTTATGGC 720
OY   597 TTGTCTGATGAAGAGCCCTGATGTACGACGACCACTTTCAGT 640
DB   721 CTGAGTGACCAACTGGCCCAAGCATGATGACACATATCCAGT 764

RESULT 14
US-09-825-012-6
; Sequence 6, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 6
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-012-6

Query Match 24.1%; Score 161.6; DB 10; Length 858;
Best Local Similarity 57.2%; Pred. No. 7.6e-42;
Matches 334; Conservative 0; Mismatches 244; Indels 6; Gaps 2;

QY 60 ACATACAACTATGTGATTAGCTCTCGCCTTGGAGAAACACATATAAAGAACAGTATGCC 119
DB 259 ACCTATCACTAGCTGTGCTAGTGAGCCACTGGAGCGACAGCTATTAAGAGGCGCTACCTG 318
QY 120 TTTCTCTATAAAGAAAGCTAGTGTCTGTAACAAAGCTACTCTACACGAA---CTAT 176
DB 319 TTCGTGTACAGGCTGACAGAGTGTCTGGGTGGACAGCTACTACTACGATGATGCTGC 378
QY 177 CAGGCTGGAGAGCGAGATGTGTTTCCAGGGAACCTTTGTGGTCTGGTTCCAGTCACCC 236
DB 379 GAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATTGTTCAGGTTCTTCTCCCG 438
QY 237 TACACCGCTGTCAGAGCTTGTGATTGTCCTCCCTGCACACACCCCTGAGACATCCGTT 296
DB 439 TTCACAGAGGTCAAGGAGTTGCCATTGTTCCCTGTCATGCGGCCCCGGGGAGCGCAGTA 498
QY 297 AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAACGTCGCTGGAATGCAGAG 356
DB 499 GCCGAGATCGACGCTCTCTATGACGCTTACCTGGATGTCAGAGAAATGGGGCTTGGAG 558
QY 357 AATTTCAATTTTCATGGTGACTTCAATGTGGCTGAGCTAGCTTCCCAAGAGGCGCTGG 416
DB 559 GACGTCATGTTGATGGGCGACTTCAATGCGGCGTGCAGCTATGTGAGACCCCTCCAGTGG 618
QY 417 AAGGACATCCGCTGAGGAGCGACCCCAAGTTTCGTTGGCTGATCGGGACCAAGAGGAC 476
DB 619 TCATCCATCCGCTGTGGACAGCCCCACCTTCCAGTGGCTGATCCCCAGACGCTGAC 678
QY 477 ACCAGGTCAGAGAGACAAACTGCGCTATGACAGGATCGTGTGTTAGAGGACAAAAT 536
DB 679 ACCACAG---CTACACCCAGCACTGTGCTATGACAGGATCGTGGTTGACGGATGCTG 735
QY 537 ATTGTCAACTCTGGTGGCTCTCAATCAACCTCGCTTTTGATTTCCAGAAAGCTTACAGG 596
DB 736 CTCGAGGGGCGGCTGTTCCGCGACTGCGCTCTTCCCTTTAACTTCCAGGCTCCCTATGCG 795
QY 597 TTGTCGAATCGAAGCGCCTGATGTCAGCGACCACTTTCAGT 640
DB 796 CTGAGTGACCAACTGGCCCAAGCCCATGAGTACCACTATCCAGT 839

RESULT 15

US-09-825-012-62
; Sequence 62, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion

US-09-825-012-62

Query Match 24.1%; Score 161.6; DB 10; Length 1548;
Best Local Similarity 57.2%; Pred. No. 1.1e-41;
Matches 334; Conservative 0; Mismatches 244; Indels 6; Gaps 2;

QY 60 ACATACAACTATGTGATTAGCTCTCGCCTTGGAGAAACACATATAAAGAACAGTATGCC 119
DB 949 ACCTATCACTAGCTGTGCTAGTGAGCCACTGGAGCGACAGCTATAAGAGGCGCTACCTG 1008
QY 120 TTTCTCTATAAAGAAAGCTAGTGTCTGTAACAAAGCTACTCTACACGAA---CTAT 176
DB 1009 TTCGTGTACAGGCTGACAGAGTGTCTGGGTGGACAGCTACTACTACGATGATGCTGC 1068
QY 177 CAGGCTGGAGAGCGAGATGTGTTTCCAGGGAACCTTTGTGGTCTGGTTCCAGTCACCC 236
DB 1069 GAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATTGTTCAGGTTCTTCTCCCG 1128
QY 237 TACACCGCTGTCAGAGCTTGTGATTGTCCTCCCTGCACACACCCCTGAGACATCCGTT 296
DB 1129 TTCACAGAGGTCAAGGAGTTGCCATTGTTCCCTGTCATGCGGCCCCGGGGAGCGCAGTA 1188
QY 297 AGAGAGATTGATGAGCTGGCTGATGTCTACACAGATGTGAACGTCGCTGGAATGCAGAG 356
DB 1189 GCCGAGATCGACGCTCTCTATGACGCTTACCTGGATGTCAGAGAAATGGGGCTTGGAG 1248
QY 357 AATTTCAATTTTCATGGTGACTTCAATGTGGCTGACGCTACGTCCTCCCAAGAGGCGCTGG 416
DB 1249 GACGTCATGTTGATGGGCGACTTCAATGCGGCGTGCAGCTATGTGAGACCCCTCCAGTGG 1308
QY 417 AAGGACATCCGCTGAGGAGCGACCCCAAGTTTCGTTGGCTGATCGGGACCAAGAGGAC 476
DB 1309 TCATCCATCCGCTGTGGACAGCCCCACCTTCCAGTGGCTGATCCCCGACAGCGCTGAC 1368
QY 477 ACCAGGTCAGAGAGAGACACAACTGCGCTATGACAGGATCGTGTGTTAGAGGACAAAAT 536
DB 1369 ACCACAG---CTACACCCAGCACTGTGCTTATGACAGGATCGTGGTTGACGGGATGCTG 1425
QY 537 ATTGTCAACTCTGGTGGTCCCTCAATCAACCTCGCTTTTGATTTCCAGAAAGCTTACAGG 596
DB 1426 CTCGAGGGGCGGTTGTTCCGCGACTCGGCTCTTCCCTTTAACTTCCAGGCTCCCTATGCG 1485
QY 597 TTGTCGAATCGAAGGCGCCTGGATGTCAGCGACCACTTTCAGT 640
DB 1486 CTGAGTGACCAACTGGCCCAAGCCCATGAGTACCACTATCCAGT 1529

Search completed: December 9, 2002, 09:24:18
Job time : 144.35 secs

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